

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 31, 2003, 21:41:08 ; Search time 76 Seconds
(without alignments)
2102.350 Million cell updates/sec

Title: US-09-857-581-66

Perfect score: 2396

Sequence: 1 MLEELALGLXVLALFXHLRP.....AHSILVCVPLARIGVASKLLS 521

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2251	93.9	1824	3	US-08-948-564-13
2	636	26.5	1781	4	US-09-499-302A-1
3	629.5	26.3	1762	3	US-08-881-784-5
4	629.5	26.3	1762	4	US-09-292-768-1
5	629.5	26.3	1762	4	US-09-292-768-65
6	627.5	26.2	1665	3	US-08-881-784-8
7	627.5	26.2	1665	4	US-09-292-768-3
8	627.5	26.2	1665	4	US-09-292-768-67
9	626.5	26.1	1685	4	US-09-292-768-69
10	625	26.1	1806	4	US-09-351-229-3
11	624.5	26.1	1762	4	US-09-292-768-63
12	617.5	25.8	1762	4	US-09-172-339-5

13	611.5	25.5	1515	4	US-09-292-768-5	Sequence 5, Appl
14	590	24.6	1657	3	US-08-948-564-11	Sequence 11, Appl
15	582.5	24.3	2174	3	US-08-606-505B-63	Sequence 63, Appl
16	582.5	24.3	2174	4	US-09-616-390-63	Sequence 63, Appl
17	581.5	24.1	1722	3	US-09-033-055A-1	Sequence 1, Appl
18	577.5	24.1	1665	1	US-08-313-075A-29	Sequence 29, Appl
19	577	24.1	1757	1	US-08-313-075A-49	Sequence 49, Appl
20	575.5	24.0	1927	3	US-08-606-505B-64	Sequence 64, Appl
21	575.5	24.0	1927	4	US-09-616-990-64	Sequence 64, Appl
22	574.5	24.0	1812	1	US-08-313-075A-37	Sequence 37, Appl
23	574.5	24.0	1824	3	US-08-606-505B-1	Sequence 1, Appl
24	574.5	24.0	1824	4	US-09-616-990-1	Sequence 1, Appl
25	572.5	23.9	1893	3	US-08-532-065B-1	Sequence 1, Appl
26	566.5	23.6	1691	3	US-08-948-564-3	Sequence 3, Appl
27	566.5	23.6	2013	4	US-09-615-192A-404	Sequence 404, App
28	564.5	23.6	1634	4	US-09-126-420A-2	Sequence 2, Appl
29	563.5	23.5	1737	4	US-09-126-420A-1	Sequence 1, Appl
30	563.5	23.5	1838	2	US-09-091-432-1	Sequence 1, Appl
31	562.5	23.5	1666	1	US-07-912-900-24	Sequence 24, Appl
32	562.5	23.5	1666	2	US-08-285-309-24	Sequence 24, Appl
33	562.5	23.5	1666	2	US-08-502-046-24	Sequence 24, Appl
34	546.5	22.8	1883	4	US-08-991-677-3	Sequence 3, Appl
35	545.5	22.8	1812	1	US-07-912-900-28	Sequence 28, Appl
36	545.5	22.8	1812	1	US-08-285-309-28	Sequence 28, Appl
37	545.5	22.8	1812	2	US-08-502-046-28	Sequence 28, Appl
38	542.5	22.6	1866	4	US-09-615-192A-103	Sequence 103, App
39	540	22.5	1755	1	US-07-912-900-29	Sequence 29, Appl
40	540	22.5	1755	2	US-08-285-309-29	Sequence 29, Appl
41	540	22.5	1755	2	US-08-502-046-29	Sequence 29, Appl
42	527	22.0	1929	4	US-09-380-420C-1	Sequence 1, Appl
43	522	21.8	1788	3	US-08-948-564-9	Sequence 9, Appl
44	483	20.2	1838	3	US-08-948-564-1	Sequence 1, Appl
45	478	19.9	1698	4	US-09-059-769-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-948-564-13
; Sequence 13, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminszky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1616
US-08-948-564-13

Alignment Scores:
Pred. No.: 4,37e-292 Length: 1824
Score: 2251.00 Matches: 451
Percent Similarity: 86.76% Conservative: 1
Best Local Similarity: 86.56% Mismatches: 69
Query Match: 93.95% Indels: 0
DB: 3 Gaps: 0

US-09-857-581-66 (1-521) x US-08-948-564-13 (1-1824)

Qy 1 MetLeuLeuCluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db 54 ATGTTGCTGACCTTGACCTTGCTGTTATGTTGGCTGCTGTTCTGCACCTTGGCTCCC 113
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db 114 ACACCCACTGCAAAATCAAAAGCACTTGGCCATCTCCCAAAACCCACCAAGCCAAAGCCT 173
Qy 41 ArgLeuProPheileGlyHis***HisLeuLeuLysAspLysLeuHisTyrAla*** 60
Db 174 CACTCTCCCTTCATAGGACACCTTCATCTCTTAAAGACAAACTTCTCCACTACGCATC 233
Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db 234 ATCGACCTCTCCAAAACATAGTCCCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 293
Qy 81 ValValAlaSerThrProcluleuPheLysLeuPheLeuGln*****CluAlaThrSer 100
Db 294 GTTGTTCCTCCACACCAAGATTGTTCAAGCTCTTCTCCAAACCCAGGACACTTCC 353
Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db 354 TTCAACACAAAGTTCCAAACCTTCAGCCATAAGACGCCCTCACCTATGATAGCTCAGTGGCC 413
Qy 121 *****Pro***ClyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
Db 414 ATGGTTCCTTCGGACCTTACTGGAAGTTGCGTGAAGAGCTCATCATGAAGACCTTCC 473
Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db 474 AAGCCACCACTGTAAACAAGTTGAGGCCCTTTGAGGACCCCAACACACCGCCAAAGTTCCTT 533
Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLeu 180
Db 534 AGGGTTATGGCCCAAGGCCAGGACGACAGGACGAGGACGAGGACGAGGAGGAGGAGGAGG 593
Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
Db 594 AAATGGACCAACAGCAGCACCATCTCCATGATGATGCTCGGGAGGCTGAGGAGATCAGAC 653
Qy 201 IleAlaArgGluValLeuLysle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db 654 ATCGCTCGGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 713
Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPhe 240
Db 714 TTGAACATCTCAGGTTGGAAGTATGAGAGAGGATCGACGACATCTTGAACAGTTC 773
Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db 774 GACCCCTGCTGTTAAAGGTTTCATCAAGAAGCGCCCTGAGATCGTGAGGAGGAGGAAGAC 833
Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280

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Db 834 GGAGAGGTTGTTGAGGTTGAGGTCAGCGGGTTCCTTGACACTTGTGTAATCGCT 893
Qy 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
Db 894 GAGGATGAGACCATGGAGATCAAAATCAACCAAGGACCATCGAGGCTTGTGTGTCGAC 953
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 954 TTTTCTCGGACGAGACAGACTCCACAGCGGTGGCAACAGAGTGGGCAATGGCAGAACTC 1013
Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
Db 1014 ATCAACAATCTTAAAGTGTGGAAAGGCTCGTGAGGAGCTTACAGTGTGTGGGAAAG 1073
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCTTACATTAGACCAATCGTGAAG 1133
Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1134 GAGACATTCGCATGTCACCGCCACCTCCCACTGGTCAAAAGAAAGTGCACAGAGAGTGT 1193
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1194 GAGATTATGATATGATGATCCAGAGGAGGACATTTGATCTCTCAATGTATGCAAGTA 1253
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1254 GGAAGACACCCCAATAACTCGGACAGACCATCGAGTTCGCTCCTCAGAGGTTCTTAGAG 1313
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1314 ACAGGGCTGAAGGGGAAGCAGGGCCCTCTTGTATCTTAGGGGCAACATTTTCAACTTCTC 1373
Qy 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1374 CCATTTGGTCTGGGAGAGAATGTGCCCTCGAGTCAATCTGGCTACTTGGGAATGGCA 1433
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db 1434 ACATTTCTGATCTCTTATTCAGTGTCTGACTTGCAGTTCAGTGTGGTCCACAGGACAG 1493
Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db 1494 ATATTGAGGTTGGTGAGCCAAAGTTAGCATGGAAGAGAGAGCGCGCTCCTACTGTCCA 1553
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db 1554 AGGCACATAGTCTTGTGTGTCTTCCACTTGCAGGATCGCGTGTGATCTAAACTCCTT 1613
Qy 521 Ser 521
Db 1614 TCT 1616

RESULT 2
US-09-499-302A-1
; Sequence 1, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; FILE OF INVENTION: INCOMPATIBLE INTERACTION
; FILE REFERENCE: 10324/P64443USO
; CURRENT APPLICATION NUMBER: US/09/499,302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1781
; TYPE: DNA

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ORGANISM: Capsicum annuum
US-09-499-302A-1

Alignment Scores: 2.66e-75 Length: 1781
Pred. No.: 636.00 Matches: 153
Score: 49.68% Conservativeness: 89
Percent Similarity: 31.42% Mismatches: 209
Best Local Similarity: 26.54% Indels: 36
Query Match: 4 Gaps: 14

US-09-857-581-66 (1-521) x US-09-499-302A-1 (1-1781)

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Qy 35 ProProSerPro***ProArgLeuProPheHleGlyHis***HisLeuLeu-----Lys 52
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Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 157 GGTCCACTTCCTCATCATGGCCTAAATAATCTAGCAAAACITTTATGGCCGCTCATGGAC 216
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Db 217 TTACAGCTGGGGAATTCCTACCTCATCATTTCTCCCGCGAATGCGGAAGGAGTA 276
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Db 277 CTAAAACTCAGAC---CTCGCTTCGCACGAGCGCGAAACTTGTGGTGGCTCACATC 333
Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheVal 131
Db 334 GTCCATTATGATAGTACGGATATATGATTTCTCCATATGTTGTAATCTGGAGGCGAGATT 393
Qy 132 ArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrValAsn***LeuArgProLeu 151
Db 394 CGTAAATTTGCTACTCTGAACTCTTAGTGCACAGATGGTCAAAATTTCTTAGCTCAATT 453
Qy 152 ArgThrGlnGlnIleArg-----Lys***LeuArg***MetAlaGln***Aglu 168
Db 454 CGCCAGGATGAGCTGCGATGATGCTCATCTATACGAACCATGCCAAATTTT----- 507
Qy 169 Ala***LysProLeuAsp***ThrGluGluLeuLysTrp***AsnSerThr***Ser 188
Db 508 -----CCGCTCAACCTTACAGACAAAATATTTTGGTTTACAAAGTTCGGTAACCTGT 558
Qy 189 MetMet***LeuGly-----GluAlaGluGluIleArgAspIleAlaArglu 204
Db 559 AGATCAGCTCTGGGAAAAATATGCTGTGACCAAGACAAACTGATAATTTTCATGAGGAA 618
Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 619 ATAATATCAATGACAGTGGAATTTAGTATGCTGATTTTCCCTACATGGAAATGCTA 678
Qy 225 ---LysValGlyLysTyrGlyLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
Db 679 CATGATGTGGTGGTTCAAAACTAGACGCTCAAGGCTCATCGTAAATCGATGAGATT 738
Qy 244 ValGluArgValIleLysLysArg***IleValArgArg***AsnGlyGlu*** 263
Db 739 TTGGAACATGATGTAATGACGACAAA-----CAGAATCGAGCGGATGGCCAAAAG 789
Qy 264 ***GluGlyGlu***SerGlyVal***Leu---AspThrLeuLeuGluPheAlaGluAsp 282
Db 790 GGTAAATGGGAATTTGGCGGTGAAGATTGATCGATGTTTCTAAGGCTTCGACAAAGT 849
Qy 283 GluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***Phe 302
Db 850 GGAGAAGTTCAATTTCCATCAGCATGATGATCAATATCAATCAATATTTAGTGGACATGTC 909
Qy 303 SerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsn 322
Db 910 TCCGCTGGATCTGAACGCTACGCACTATAAATTTGGCCATTTAGTCAAAATGATGAG 969

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Qy 323 AsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp*** 342
Db 970 AAACCAAGTGTCTTAGCAAAAGGCACAGCTGAAGTGAAGCAAGTCTTGAAGGAAAGAAA 1029
Qy 343 LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThr 362
Db 1030 GGTTTTCACAAATTTGATCTTGATGAGTGAAGTACTTGAAGTAGTAATCAAGAAACT 1089
Qy 363 PheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys*** 381
Db 1090 CTAAGGATGCACCTCCCAATTCCTCTATTAGTCCCTAGAGAATCTATGAAGGATACAAAG 1149
Qy 382 IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTyrGlnValGly 401
Db 1150 ATTACGGGTACATATATACCTTTCAAAACTCGAGTCATAGTTAATGATGGCAATTGGA 1209
Qy 402 ***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr 421
Db 1210 CGAGATCCTGAAAGTTGGGATGACCCCTGAAAGCTTTTCCCCAGAGAGATTC----- 1260
Qy 422 ***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuPro 441
Db 1261 -----GAGAATAGTCTGTGACTTTCTTGGAAAGCCATCATCAATTTATTTCCA 1308
Qy 442 PheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThr 461
Db 1309 TTTGGTGGGGAAGAGGATTTGCTCTGGAATGCTTTTGGTTAGCCAATGTTGGACAA 1368
Qy 462 LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIle 481
Db 1369 CCATTAGCTCAATTTACTTTATCACTTCGATCGGAAACTC-----CCTAATGACAAAGT 1422
Qy 482 LeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArg 501
Db 1423 CACGAAATTTGGAC-----ATCAGGAGTCACTGGAATTTCTGCAACAAGA 1470
Qy 502 AlaHisSerLeuValCysVal 508
Db 1471 AAGGATGATCTTGTGTTGATT 1491

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RESULT 3

US-08-881-784-5
Sequence 5, Application US/08881784
Patent No. 6083731

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: Kaip, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
ADDRESS: PLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,784
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: WSU19777
TELECOMMUNICATION INFORMATION:

; CURRENT APPLICATION NUMBER: US/09/292,768
 ; CURRENT FILING DATE: 1999-04-14
 ; EARLIER APPLICATION NUMBER: 08/881,784
 ; EARLIER FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1
 ; LENGTH: 1762
 ; TYPE: DNA
 ; ORGANISM: Mentha spicata
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (20)..(1507)
 ; US-09-292-768-1

Alignment Scores:
 Pred. No.: 1,95e-74 Length: 1762
 Score: 629.50 Matches: 148
 Percent Similarity: 48.79% Conservative: 93
 Best Local Similarity: 29.96% Mismatches: 212
 Query Match: 26.27% Indels: 41
 DB: Gaps: 14

US-09-857-581-66 (1-521) x US-09-292-768-1 (1-1762)

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Qy 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
Db 101 TCGAATCCCAACAAACCTA-----CCTCCGAGCCCT---CCGAGCTGCCGGTGATC 151
Qy 46 GlyHis***HisLeuLysAspLysLeuHisTyrAla***IleAspLeuSerLys 65
Db 152 GCGCACCTCCACTCTCTGGGGAGGCTTCCCGAGCAGCGTGTAGGAGCATAGCCAG 211
Qy 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
Db 212 AAGTACGGCGCGTGGCCACGCTGAGCTGGGAGAGTGACTCGGTGGTGCTGCTCGTCG 271
Qy 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 272 GCGGAGGCGGAGGAGGAGCGGAGCTGAAGGTGCTGGAC---CCGAACCTTCGCGGCGGTTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyraSP-----ValAla*****Pro*** 124
Db 329 GAGGCATCGGTCGAGGACCATGGTACGACAAAGATGACATCATCTTCAGCCCTAC 388
Qy 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
Db 389 AACGATCACTGGCGGCACATCGGAGGATCTGCTGACAGAGCTGCTGAGCCCGAGAAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 449 GTCAGTCTTCGGGTACATAGCAGGAGGAGATCGAGCGCCCTCATCGGCTCTCGGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
Db 509 TCGTCGGGGGAGCG-----CCGCTGACGTGAGGAGGAGGTGTCGAGATGCTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Db 563 GTCGTGTGTGCGAGCGCGCGCTTCGGGAGTGTGCTCAAGGACCGAGGTTGCTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGlnTyrSerLeuThrAspPheIle***Pro 220
Db 623 TTGTGTAGAGGAGTCCCTGCGCATTTGGCTCCGGGTTTGAGCTGGCGGAT---CTCATCCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
Db 680 TCCTCATGGCTCCCTCAACCTGCTAGTTGAAACAGTAC-----AGGTTGACAGGATG 733
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 734 CCGCGCGCCCTCGATCATCATCTTGTATGGGTTCCTGGAGGAGCATAGG----- 781
  
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Qy 257 ArgArg***AsnGlyGlu*****GluGlyVal***SerGlyVal***Leu---AspThr 275
Db 782 -----GAGANAAGACGGCGAGTTTGGAGCGAGACATCTCGTGCAGTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys 295
Db 827 CTTTTCAGGATGAGAGAGGCGAGCATCAAAATTCCTACTTCCATTCATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTTP 315
Db 887 GGTTCATTTTCGACACCTTCTCCGGGGAGCTGAACGCTTCGAGCACCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Db 947 GCGTTGTCGAACTGATGAGGAATCCGGGAGAGTGCACCAAGTGCAGCGGAGGTAAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
Db 1007 GAGCGCTCAAGGAAAGACAGCTGTGGATTGAGCGAGGTGCGAAGAGCTAAATACCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProLeuProValValLysArgLys 375
Db 1067 AGATCGGTGTTAAAGAGAGCTCTGAGGCTGCACCTCCCTTTCCATTAAATCCCAAGACA 1126
Qy 376 Cys***GluLysCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Db 1127 TCAGGAGAGATTCGAGGTAAACGGGTACAGATTCCGGCCAAAACACTAGAATCTTCATC 1186
Qy 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
Db 1187 AACGTCTGGCTATCGGAAGGATCCCAATACTACTGGGAAGATCCGACACCTCCGCTC 1246
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
Db 1247 GAGAGATTGATGAGGTTCAGG-----GATTTCATGGGAAC 1285
Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db 1286 GATTCGAGTTCATCCATTCGGGCGGTGCGAAGATTCGCCCGTTTACATTCGGG 1345
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Db 1346 CTGCGAAATGTTGAGATCCCATTCGGCAACTGCTTACCACCTTCGACTGGAATG--- 1402
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
Db 1403 ---CCACAGGAATG-----ACTGATCGCGACTTGGACATGACGAGACCCCA 1447
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db 1448 GGTCTTTCTGGGCCAAAAGAAAATGTTTGTCTGGTCCC 1489
  
```

RESULT 5

US-09-292-768-65
 ; Sequence 65, Application US/09292768
 ; Patent No. 6194185
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B
 ; APPLICANT: Lupien, Shari L
 ; APPLICANT: Karp, Frank
 ; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
 ; FILE REFERENCE: wsuri3463
 ; CURRENT APPLICATION NUMBER: US/09/292,768
 ; CURRENT FILING DATE: 1999-04-14
 ; EARLIER APPLICATION NUMBER: 08/881,784
 ; EARLIER FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 65
 ; LENGTH: 1762
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence

```

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1762)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: spearmint limonene-6-hydroxylase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
US-09-292-768-65

Alignment Scores:
Pred. No.: 1,95e-74 Length: 1762
Score: 629.50 Matches: 148
Percent Similarity: 48.79% Conservative: 93
Best Local Similarity: 29.96% Mismatches: 212
Query Match: 26.27% Indels: 41
DB: 4 Gaps: 14

US-09-857-581-66 (1-521) x US-09-292-768-65 (1-1762)
QY 26 SerLysAlaLeuAlaHisLeuProAsnProSerPro***ProArgLeuProPheile 45
DB 101 TCGAATCCCAACAACTA-----CTCGAGCCCT---CCGAGCTGCCGTGATC 151
QY 46 GlyHis***HisLeuLeuLysAspLysLeuHisTyrAla***IleAspLeuSerLys 65
DB 152 GCCACCTCCACTTCTGCGGAGGCTTCCACAGCAGTGTTCAGGAGCATAGCCAG 211
QY 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
DB 212 AAGTACGGCCGCGTCCGACCTGAGCTGGAGAGTGTACTCGTGTGCTGCTGCG 271
QY 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
DB 272 GCGGAGGCGCAGCAGCAGCGATGAAGTGTGGAC--CCGAACTTCGCGCAGCGGTC 328
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
DB 329 GACGCGATCGGTCGACGACCATGTGGTACGACAAAGATGATCACTTCAGCCCTAC 388
QY 125 GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeuLeuAsnAlaThrThr 144
DB 389 AACGATCACTGCGCCAGATCGGAGGATCTCGGTGACAGAGCTGCTGAGCCCGAAGAC 448
QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
DB 449 GTCAGGTCTCTGGGTACATAGGCGAGGAGATCGAGCGCCCTCATCCGCTGCTCGG 508
QY 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
DB 509 TCGTCGGGGGAGCG-----CCGTGACGTGACGAGGAGGTGTCGAAGATGCTGTGT 562
QY 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
DB 563 GTCGTCGTGTGACGGCGCGCTTCGCGAGTGTGTCAAGGACCAGCGGTTCGTTGGCGGAG 622
QY 201 IleAlaArgGluValLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 220
DB 623 TTGTTGAGGAGTCTGCTGCACTGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTC 679
QY 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
DB 680 TCTCATGCTGCTCAACCTGCTAGCTTGAACAGTAC-----AGGTTGACAGGATG 733
QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysLysLysLysLysLysLys 256
DB 734 CCGCCCGCGCTGCTACATCTTCTGAGGAGGATGAG----- 781
QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu--AspThr 275

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DB 782 -----GAGAGAGAGCGCGAGTTTGGAGCGGAGGACATCGTCGACGTT 826
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys***IleLys 295
DB 827 CTTTTCAGGATGCGAAGAGCGGACGACATCAAAATTCCTTCCAAATTCGATCAAG 886
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla***ThrGluTyr 315
DB 887 GGTTCATTTTCGACACCTTCTCCGCGGAGCGTGAACGCTTCGACGACCATCTCATGG 946
QY 316 AlaLeuAlaLeuLeuLeuAsnPro***ValLeu***AlaArgGluGlu***Tyr 335
DB 947 GCCTTGTGGAAGTGTAGGAATCGGCGGAGTGCACCAAGTGCAGCGGAGGTGAAGA 1006
QY 336 SerValValGlyLysAsp***LeuValAspGluValAlaThrGlnAsnLeuProTyrIle 355
DB 1007 GAGCGCTCAAGGGAAGACAGTCGTGGATTTCAGCGAGGTGCAAGAGTAAATACCTG 1066
QY 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
DB 1067 AGATCGGTGTAAAGGAGACTCTGAGGCTGCACCTCCCTTTCCATTAATCCAGACAA 1126
QY 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
DB 1127 TCAGGGAAGATGCGAGGTACAGGATTCGCGCCAAACTAGAAATCTTCATC 1186
QY 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
DB 1187 AAGCTGTGGCTATCGGAGGATCCCAATACTGGAAGATCCCGACACCTTCGCGCT 1246
QY 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
DB 1247 GAGAGATTCATGAGGTTCGAG-----GATTTCATGGGAAC 1285
QY 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
DB 1286 GATTTCGAGTTTATCCATTCGCGGCGGTCGAAGAATTCGCCCGGTTTACATTCGGG 1345
QY 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
DB 1346 CTGCAAAATTTGAGATCCCATTTGGCGCACTGCTACCATTCGACTCGGAATTTG--- 1402
QY 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
DB 1403 ---CCACAGGAATG-----ACTGATGCGGACTTGGACATGACGAGAGCCCA 1447
QY 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
DB 1448 GGTCTTCTGGGCCAAAGAAAATGTTGCTGTTGCC 1489

RESULT 6
US-08-881-784-8
; Sequence 8, Application US/08881784
; Patent No. 6083731
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Lupien, Shari L.
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
; THE PRODUCTION OF LIMONENE HYDROXYLASES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; ADDRESSEE: PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/881,784
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Shelton, Dennis K.
 REGISTRATION NUMBER: 26,997
 REFERENCE/DOCKET NUMBER: WSUR19777
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 224-0718
 TELEFAX: (206) 224-0779
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Mentha x piperita
 IMMEDIATE SOURCE:
 CLONE: pPM17
 US-08-881-784-8

Alignment Scores:
 Pred. No.: 3,336-74 Length: 1665
 Score: 627.50 Matches: 147
 Percent Similarity: 48.17% Conservative: 90
 Best Local Similarity: 29.88% Mismatches: 204
 Query Match: 26.19% Indels: 51
 DB: 3 Gaps: 11

US-09-857-581-66 (1-521) x US-08-881-784-8 (1-1665)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
 DB 124 CTTCCGGGCGCG---CCGAAGCTCCGCTGATCGGCGACCTCCACCTCTTATGGGGAAG 180
 QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
 DB 181 CTGCGCGACGACGGCG 240
 QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLeuLysLeuGln 94
 DB 241 CTCGCGAGGTGCTCTCGTCTGCTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCT 300
 QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
 DB 301 CTGTGTGAC---CCGGCTGCGCGACCGGTTCTGAGAGCATCGGCGACGAAGATCATGTGG 357
 QY 115 TyrAsp-----ValAla*****Pro***GlyProThrTrp***PheValArgLys 133
 DB 358 TAGCACAACGACGACATCATCTTCAGCCCTTACAGCGTGCATCGCGCGCGCGCGCGCGCG 417
 QY 134 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
 DB 418 ATCTCGGCTCCGAGCTCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477
 QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
 DB 478 GACGAGGTGTCCTCGGCGACCTCCGCTCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 537
 QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
 DB 538 GACCTCAGGACGCGATAGCGACGCTGCTGCTCCATCATCTCTCGCGCGCGCGCGCGCGCG 597
 QY 194 -----GluAlaGluIleArgAspIleAlaArgGluValLeuLysIle*** 209
 DB 598 AGCGTGATCAGGACGACGAGCTGTGTGAGCTGTGTGAGGACGCGCGCGCGCGCGCGCGCG 657
 QY 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224

DB 658 TCCGGGTTCAGCTCCCGGACATGTTCCCTCTCTCAAGCTCTCAACTTCTCTCTCTCTCTG 717
 QY 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
 DB 718 AACAAAGCAAGCTGTGGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
 QY 242 ProValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 261
 DB 775 ---GTGAGGAGCACAAGCTCAAGAG----- 798
 QY 262 Glu*****GluGlyGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
 DB 799 -----AGCGCGAGTTTGGCGGAGGACATATTACACTCTTTAGGATGCAG 849
 QY 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
 DB 850 AAGATAGCCAGATCAAGTCCCATCAACCAAGCCCATCAAGCCCTTCATCTTCGAG 909
 QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 DB 910 ACGTCTCTCAGCGGCGGACGAGACATCATCAACCAAGCCCTGTGGGTGATGCGGAGCTG 969
 QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 DB 970 ATGAGGAATCCAGAGGTGATGGCGAAGCGCGGAGGTGAGCGCGCTGAAGGGG 1029
 QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProThrIleArgAlaIleValLys 360
 DB 1030 AAGACGAGCTGGGACGTCGAGCGACGTGCAGGAGCTTAAGTACATGAATCGGTGGTGAAG 1089
 QY 361 GluThrPheArgMethHisProProLeuProValValLysArgLysCys***GluGluCys 380
 DB 1090 GAGACGATGAGGATGCACCTCCGATCCCGGTTCATCCGAGATCATGCGAGAGAAGATCC 1149
 QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
 DB 1150 GAGGTCAACGGGTACAGATTCGGAATAAGCGCAGATCATCATCACTGTGGTCCATG 1209
 QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 DB 1210 GGTAGAAATCTCTCTACTGGGAAACCCGAGACCTTTTGGCCGCGAAAGGTTT----- 1263
 QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 DB 1264 -----CACCAAGTCTCGAGGATTTTCATGCGAAGCATTCGAGTTCATC 1308
 QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 DB 1309 CCATTTGGAGCTGGAAGAAGATCTCCCGCGTTTGAATTCGGGTTCGCAATGTTGAG 1368
 QY 461 ThrLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
 DB 1369 GTCCCATTTGGCAGCTCTTTTACCACTTCGACTGGAAGTTGGCGGAAGGAATGACCT 1428
 QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGluLeu 497
 DB 1429 -----TCCGATATGACATGCTCTCAGCAGCAGAGGCTT 1461
 QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
 DB 1462 ACCGGAATAGAAAGAACATCTTCTACTCTCTCC 1497

RESULT 7

US-09-292-768-3
 ; Sequence 3, Application US/09292768
 ; Patent No. 6194185
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B
 ; APPLICANT: Lupien, Shari L
 ; APPLICANT: Karp, Frank
 ; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
 ; TITLE OF INVENTION: LIMONENE HYDROXYLASES

```

; FILE REFERENCE: wsurl3463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Mentha piperita
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
; US-09-292-768-3

Alignment Scores:
Pred. No.: 3,33e-74 Length: 1665
Score: 627.50 Matches: 147
Percent Similarity: 48.17% Conservative: 90
Best Local Similarity: 29.88% Mismatches: 204
Query Match: 26.19% Indels: 51
DB: 4 Gaps: 11

US-09-857-581-66 (1-521) x US-09-292-768-3 (1-1665)

QY 35 ProProSerPro***ProArgLeuProPheleGlyHis***HisLeuLeuLysAspLys 54
DB 124 CTCCTCGGCGCCG---CCGAAGCTCGCTGATCGGCGACCTCCACCTCTATGGGGAAAG 180
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
DB 181 CFCGCGCAGCAGCGCTGCCAGCTGCGGAGCAGTAGCGGCCAGTGGCCCGCCAGTCGAG 240
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLeuLysLeuGln 94
DB 241 CFCGCGCAGGTTCTCCGCTGCTGCTCGCCGCGAGCGCCAGCAGGCGCGATGAAG 300
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 301 CFTGTGGAC---CCGGCTCGCGCGGCGGCTCGAGACGATCGGCGACGATCATGTGG 357
QY 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 358 TACGACACGAGGACATCATCTTCAGCCCTACAGCGTCCATCGCGCCAGCAGCGCGAAG 417
QY 134 LeuIleMetAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 418 ATCTCGGTCTCGAGCTCTCTCAGCGCCGCGACGTCCTCGCTCCCTTCGCGCTTCATCAGCAG 477
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 478 GACGAGGTCTCCGCTCTCCGCGCACCTCGCTCTCCGCGCGCGCGCGCGCGCGGTG 537
QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 538 GACCTCAGGCGGATACGACGCTGACGCTGCTCCATCATCTCAGCGCGCGCTTCGGG 597
QY 194 -----GluAlaGluGluLeuLeuArgAspIleAlaArgGluValLeuLysLys*** 209
DB 598 AGCGTGATCAGGACACGAGGAGTGTGTGAGCTGTGTGAAGAGCGCGCTCAGCATGCGG 657
QY 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
DB 658 TCCGGTTCGAGCTCGCGGACATGTTCCCTCTCCAGCTCCCTCACTTCTGCTGTGG 717
QY 225 -----LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAsp 241
DB 718 AACAGACGACGCTGTGGAGGATGCGCGCGCTGCGAGCCATCTCTCGAGGCCATC--- 774
QY 242 ProValValGluArgValIleLysLysArg***IleValArgArg***AsnGly 261
DB 775 ----GTGGAGGACACAGCTCAAGAG----- 798

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QY 262 Glu*****GluGlyGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
DB 799 -----AGCGCGAGTTTGGCGGAGGACATTAATGACGACTCTTCTTAGGATGAG 849
QY 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
DB 850 AAGGATAGCCAGATCAAGATCCCATCACCACCAAGCCATCAAGCCCTTCTTCGAC 909
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
DB 910 ACCTTCTCAGCGGCGGAGCAGCATCAACACCACCCCTGTGGGTGAGTGGCGAGCTG 969
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 970 ATGAGGAATCCAGAGGTGATGGCGAAGCGCAGCGGAGTGCAGAGCGCGCTGAAGGGG 1029
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1030 AAGACGAGCTGGGAGCTGGACGACGTCGAGGAGCTTAAGTACATGAATCGGTGTGAAG 1089
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
DB 1090 GAGACGATGAGGATGCACCTCCGATCCGCTTCATCCCGAGATCATGCAGAGAGAATGC 1149
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
DB 1150 GAGGTCAACGCGGTACACGATTCGGAATAAGCGCAGAAATCATGATCAACGTGGTCCATG 1209
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1210 GTTAGGAATCTCTCTACTGGGAAACCCGAGACCTTTTGGCCCGAAAGTTT----- 1263
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1264 -----GACCAAGTCTCGAGGATTTTCATGCGGAACGATTTCGAGTTTCATC 1308
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1309 CCATTTGGAGCTGGAAGAAATCTGCCCGGTTGAATTCGGGTGGCAATGTTGAG 1368
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
DB 1369 GTCCCATTTGCGACAGCTTCTTTACCACTTCGACTGGAGTGGCGGAGGAATGACCCCT 1428
QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
DB 1429 -----TCGATATGACATGTCTGAGCGCAGAGGCCCTT 1461
QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
DB 1462 ACCGGAATAAGAAAGAACAACTCTCTACTCGTTCC 1497

RESULT 8
US-09-292-768-67
; Sequence 67, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wsurl3463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 67
; LENGTH: 1665
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-3-hydroxylase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1665)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-3-hydroxylase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
US-09-292-768-67

Alignment Scores:
Pred. No.:      3,33e-74      Length:      1665
Score:          627.50      Matches:      147
Percent Similarity: 48.17%      Conservative: 90
Best Local Similarity: 29.88%      Mismatches: 204
Query Match:      26.19%      Indels:      51
DB:               4          Gaps:        11

US-09-857-581-66 (1-521) x US-09-292-768-67 (1-1665)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 CTTCCGGGCGCG---CCGAAGTGGCGGTGATCGGGCACCTCCACCTCTATGGGGGAG 180

QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer***** 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CTGCCGCACACGCGTCCGACGCGTGGGAGAGTAGTACGGCCGACGTGGCCAGCTGGCAG 240

QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CTCGCGGAGGTCTTCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CTGGTGGAC---CCGGCTGCGCGGACCGTTTCGAGACATCGGACGACGACGACGACGACG 357

QY 115 TyrAsp-----*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 TAGCACACGACGACATCATCTTCAGCCCTCAGCGCTGCACTGGCGCACGATGGCGGAG 417

QY 134 LeuIleMetAsnAspLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 ATCTGCTCTCGAGCTCTCAGCCGCCACAGCTCCGCTCTTCGCTCTTCATCAGGCGAG 477

QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 GACGAGGTCTCCGCTCTCCGCGCCACCTCCGCTCTCCGCGCGCGCGCGCGCGCGCGCG 537

QY 174 Asp***ThrGluLeuLeuLysTyr***AsnSerThr***SerMetMet***LeuGly 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 GACCTCAGCGAGGATACGACGCTGCTCCATCATCTCGAGCGCGCGCGGTTCGCGG 597

QY 194 -----GluAlaGluIleArgAspIleAlaArgGluValLeuLysIle*** 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 AGCGTGATCAGGACACGACGAGGTGGTGAGCTGGTCAAGGACGCGCTCAGATGCGG 657

QY 210 GlyGlyTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 TCGGGTTCGAGCTCGCCGACATGTTCCTCTCCCAAGCTCTCAAGTCTGCTGCTGCTGCTG 717

QY 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 AACAGACGACGCTGAGGATGGCGCGCGCGCTCGACGCCATCTCTGAGGCCATC--- 774

QY 242 ProValValGluArgValIleLysLysArgArg***IleValArgArg***AsnGly 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 775 ---GTGGAGGACGACAAAGCTCAAGAG----- 798

```

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QY 262 Glu*****GluGlyGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 799 -----ACCGCGAGTTTGGCGGAGACATATTGACGTACTCTTTAGGATCAG 849

QY 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 850 AAGGATAGCCAGATCAAGTCCCATCACCACCAAGCCATCAAGCCATCATCTCTCGAC 909

QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 910 ACGTTCTCAGGGGACCGAGACATCAACACCACCTCGTGGGTGATGGGGAGCTG 969

QY 321 IleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLys 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 970 ATGAGGAATCCAGAGGTGATGTCGCGAAAGCGCAGCGGAGGTGAGAGCGGCGTGAAGGG 1029

QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1030 AAGACGAGTGGGACGTGGACGCGTGCAGGAGCTTAAGTACATGAATCGGTGGTGAAG 1089

QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1090 GAGACGATGAGATGCACCTCCGATCCGTTGATCCCGAGATCATGCGAGAGAATGC 1149

QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1150 GAGTCAACGGGTACACGATTCGGAATAGCCAGATCATGATCAACGTGTGTCATG 1209

QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 GTAGGATCTCTCTACTCGGAAACCCGAGACCTTTTGGCCCGAAAGSTTT----- 1263

QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1264 -----GACCAAGTCTCGAGGATTCATGGAACGATTCGAGATTCGAGTTCATC 1308

QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1309 CCATTGAGCTGGAAGAAGATCTGCCCGSTTGAATTCGGGTGGCAATGTTCAG 1368

QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1369 GTCCCATTTGGCACAGCTCTTACCACTTCGACTGGAAGTTGGCGGAAGGATGAACCT 1428

QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1429 -----TCCGATATGGACATGCTCTGAGGCGAGAGGCCCTT 1461

QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1462 ACCGGAATAAGAAAGAACATCTTCTACTGTTCCC 1497

RESULT 9
US-09-292-768-69
; Sequence 69, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: WSUR13463
; CURRENT APPLICATION NUMBER: US/09/292.768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881.784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Artificial Sequence

```


Pred. No.: 8.14e-74 Length: 1806
Score: 625.00 Matches: 165
Percent Similarity: 50.60% Conservative: 90
Best Local Similarity: 32.74% Mismatches: 198
Query Match: 26.09% Indels: 52
DS: 4 Gaps: 13

US-09-857-581-66 (1-521) x US-09-351-229-3 (1-1806)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 86 CGCGCGGCCCCAACCA---TGGCGGATCATCGGCAACCTTAACCTCATG---GGCGAG 139
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer***** 74
DB 140 CTGCCCCACCGCTCCATGAACAGCTCTCCAAAGCGGTACGGTCCCTCATGAGCTCTGG 199
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
DB 200 TTGGGTGCTGCTGCTGCTGCGCGCTCCGCGAGATGGCAAGCTCTTCTCTCAAG 259
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 260 ACCAACGACGCG---CGCTTCCGACCGCGCGAGGTTCCGAGTCGCGCAAGTACACCGCG 316
QY 115 TyrAsp-*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 317 TAGGACTGCTCGGCGCTCTGCTGCGCTCTTTTGGCGGTACTGCGCGACGCGACGCGAG 376
QY 134 LeuIleMetAsnAspLeuLeuAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 377 ATCTGCGCCACCGAGCTCTCAGCGCCGCGCTCGAGTCTTCGAGCATCTCGCGAC 436
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 437 GAGGAGTCCGCGTATGCTGCGAGCTGCGCGACGCTGCGCGACGCGCGCGCTT 496
QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 497 AGGGACTACTCGAGATGTG-----GGCTCGCGGTGATCTCGGATAGTCTTCTGGGC 550
QY 194 Glu----- 194
DB 551 AAGAGTACGTATGAGGAGCGCGGAGCGGTGAGGGGAGCTCAGCGCGCGATAACG 610
QY 195 AlaGluGluIleArgAspIleAlaArgGluValLeuLysIle**GlyLeuTyrSerLeu 214
DB 611 CTGCGCGAGTTCAGGAGATGTGGACGAGTCTTCGCGCTTCACGGTTCGGTTAACATT 670
QY 215 ThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAsp 234
DB 671 GGTGATTATATCCCTTGGCTAGATTGGCTGGACCTGCAGGGCTACGTTGCTAGGATGA 730
QY 235 AspIleLeuAsnLysPheAspProValValGluArgValIle-----LysLysArg 251
DB 731 AGAATGAAGCGAGGTTGGTCGATTCCTGGAACGAGCTTGGAGCGTGCACACAGCGCG 790
QY 252 Arg***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal 271
DB 791 CGACTA-----CGCGAGGAGGAACTTGTGGCAAGAGAT----- 826
QY 272 ***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
DB 827 ATGTTGGAGCTGCTGCTGCGAGTCCGCGCTACACTAGTCTTTGAAGTCCAGCTCAGCAG 886
QY 292 *****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
DB 887 GACAATGTTAAGCTATCACAGACCTAATCATCGGAGCGACCGATAGTAATCCAAC 946
QY 312 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331
DB 947 AGCGTGAAGTGGCTGCTCGGAGTCTCTCAAGAACCTCTAGATCTTAGCAAGCCCATG 1006

QY 332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsn 351
DB 1007 GAGGAGCTGAACCATGTATAGCCGCGAGCGACTGTGTAGCGAAACGCGACTCCCT-CGC 1065
QY 352 LeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProVal 371
DB 1066 CTCCCTCATCATCGAGGTGTCTCAAGGAGACCATGCGCTGACCATGCGCGCGGATG 1125
QY 372 Val---LysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGly 390
DB 1126 CTGCACCCACGTCGGCGCGGAGACATCTCGACGGATACGACGTCGCTCGCTGGC 1185
QY 391 AlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgPro 410
DB 1186 ACGTCTTGTTCATCAACGTGTGGCAATCGCGCGGACCTTGACGTGTGGAGCGCGCG 1245
QY 411 SerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****Leu 430
DB 1246 GAGGAGTTCGCGCGGAGCGGTTCTGTCGAGAGC-----AAGATC 1284
QY 431 AspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysPro 450
DB 1285 GACGTGAGGCGCATGACTTCCAGCTGCTCGCGTTCGCTGCGCGGCGAATGTGCCCC 1344
QY 451 GlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPhe 470
DB 1345 GGGATCAACCTCGCGCTAAAGGTGATGGCTTGGCAATCTGCCAATCTGTACACGGCTC 1404
QY 471 AspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSer 490
DB 1405 GAGTGGAGGCTT-----CGGAGCGGTGACGCGCAGAG-----GAGCTGAGC 1446
QY 491 -MetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLe 510
DB 1447 CATGATGAGCGCTTCAAGCTCGCGTACGCGGTAATCCCGTATGCTGCTGCGCGCA 1506
QY 510 uAlaArgIle 513
DB 1507 GCCCAGGTG 1516

RESULT 11
US-09-292-768-63
; Sequence 63, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: WSUR13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
; OTHER INFORMATION: Computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase variant
US-09-292-768-63
Alignment Scores:
Pred. No.: 9.16e-74 Length: 1762

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Score: 624.50 Matches: 147
Percent Similarity: 47.99% Conservative: 92
Best Local Similarity: 29.52% Mismatches: 210
Query Match: 26.06% Indels: 49
DB: 4 Gaps: 13

US-09-857-581-66 (1-521) x US-09-292-768-63 (1-1762)

Qy 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheLe 45
Db 101 TCGAATCCCAACAAACCTA-----CCTCGAGCCCT--CCGAAGTCGCGGTGATC 151
Qy 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Db 152 GGCACCTCCACTTCCTGTGGGAGGGCTTCCCGACGCTGTATAGGAGCATGCCAG 211
Qy 66 LysHisGlyProLeuPheSer***PheGlySerMetProThrValValAlaSerThr 85
Db 212 AAGTACGGCGCGTGGCGCAGCTGCAGTGGGAGAGTGTACTCGTGTGTCTGCTGCG 271
Qy 86 ProGluLeuPheLysLeuPheLeuGln***GluAlaThrSerPhe***ThrArgPhe 105
Db 272 GCGAGGCGCAGCAGCAGCGATGAAGTCTCTGGAC---CCGAACCTCGCCGACCGGTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAlaAla***Pro*** 124
Db 329 CAGCGCATCGGTCCAGGACCATGTGTCAGCAAGATGACATCATCTTCAGCCCTTAC 388
Qy 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAlaThrThr 144
Db 389 AAGCATCACTGGCGCCAGCGATCGGAGGATCTGTCGACAGAGCTGTGAGCCGGAAGAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 449 GTACGTCCTTCGGGTACATAAGACAGGAGGATCGAGCGCTCATCCGCTGTCGCGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
Db 509 TCGTCGGGGGAGCG-----CCGTCGAGCTGACGAGGAGGAGTGTGCGAAGATGTCGTG 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Db 563 GTGCTGCTGTGAGGGCGGTTCGGAGGTGCTCAAGACACGAGGCTCGTTCGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGlyTyrSerLeuThrAspPhe----- 217
Db 623 TTGCTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 682
Qy 218 -----Ile***ProLeuLys***LeuLysValGlyLysTyrGluLysArg 232
Db 683 TCATGGCTCTCAACCTGCTAGCTTGAACACATACAGGTTCGAGAGGATGCGCCGCC 742
Qy 233 IleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArg 252
Db 743 CTCGATCACATCTTGATGGTTC-----CTGGAGGAGCATAGG 781
Qy 253 ***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal*** 272
Db 782 -----GAGAAGAACGCGCGGAGTTCGAGCGGAGGAC 814
Qy 273 Leu---AspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
Db 815 ATCTCGACCTTCTTTTCAGAGTCACAGAGGCGGACATCAAAATTCCTTACTTCTCC 874
Qy 292 *****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
Db 875 AATTGCATCAAGGGTTTCATTTTCGACACCTTCTCGCGGGAGCTGAACGCTCTTCGAG 934
Qy 312 ***ThrGlnTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331
Db 935 ACCATCTCAGGGCGGTGTGCGAACTGATGAGAAATCCGCGGAGATGCCAAGGTCCAG 994
Qy 332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsn 351
```

RESULT 12

```
US-09-172-339-5
; Sequence 5, Application US/09172339
; Patent No. 6291745
; GENERAL INFORMATION:
; APPLICANT: Eucalire Meyer, Terry
; APPLICANT: kaipani, Nasser
; TITLE OF INVENTION: Limonene and Other Downstream
; TITLE OF INVENTION: Metabolites of Geranyl Pyrophosphate for Insect Control in
; FILE REFERENCE: 5718-65
; CURRENT APPLICATION NUMBER: US/09/172,339
; EARLIER FILING DATE: 1998-10-14
; EARLIER APPLICATION NUMBER: 08/449,061
; EARLIER FILING DATE: 1995-05-24
; EARLIER APPLICATION NUMBER: 08/153,544
; EARLIER FILING DATE: 1993-11-16
; EARLIER APPLICATION NUMBER: 08/042,199
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Mentha spicata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Carveol Synthase
; NAME/KEY: CDS
; LOCATION: (20)...(1507)
US-09-172-339-5

Alignment Scores: 7,978-73 Length: 1762
Pred. No.: 617.50 Matches: 145
Score: 48.58% Conservative: 95
```


Qy	55	LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer*****74
Db	163	CTCCCGACAGCAGCGTGGCCAGCGTGGGAAGAGTAGCGCCGCTGCCACAGTCGAC222
Qy	75	PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGlu94
Db	223	CTGGGTGAGGTGTTCCGTCGTCCTTTCGTCGGGAGGCGAGGAGGCGGTGAC282
Qy	95	*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr114
Db	283	CTGGTAGAC---CCGGCGTGGCGGAACCGGTCGAGAGCATCGGACAGAGGATCATGTGG339
Qy	115	TyrAsp---*****ValAla*****Pro**GlyProTyrThr**PheValArgLys133
Db	340	TACACACACGAGACATCATCTTCAGCCCTACAGCGAGCCTGGGCCAGATGCCGCAAG399
Qy	134	LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr153
Db	400	ATTCGGCTCCGAGCTCTCTCTCCGCAACGTCGCTCGCTTCGCTTCATCCGGCAG459
Qy	154	GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu173
Db	460	GAGCAGGTGCGGGCTCTCCGCCACCTCCGCTCTCGCAGCAGGGCGGCC-----GTG513
Qy	174	Asp***ThrGluGluLeuLeuLysTyr**AsnSerThr***SerMetMet***LeuGly193
Db	514	GACATGACGGAGGATAGACGCTGACGTGCTCCATCATCTCGAGGCGCGCTTCGGG573
Qy	194	GluAlaGluLulleArgasp-----IleAlaArgGluValLeuLys207
Db	574	AGCGTG-----ATCAGGCAACACGGCGAGCTGCTGGGCGTGTCAAGCAGCGCTCAGC627
Qy	208	Ile**GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu-----224
Db	628	ATGGCCTCGGGGTTCGAGCTCGCGACATGTTCCCTCTCCCAAGCTCTCAACCTCCTC687
Qy	225	-----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLys239
Db	688	TGCTGTGAACAAGACAGCAAGCTCTGGAGGATCGCGCGCGCTCGACACCATCTCTCAGGCC747
Qy	240	PheAspProValValGluArgValIleLysLysArgArg**IleValArgArgArg***259
Db	748	ATC-----GTCACGAGCACAGTTCACAGAG-----774
Qy	260	AsnGlyGlu*****GluGlyGlu***SerGlyVal---***LeuAspThrLeuLeuGlu278
Db	775	-----ACGCGCAGATTTCGGCGCGGAGGACATCATCGACGCTCTCTTCAGG819
Qy	279	PheAlaGluAspGluThr**GluIleLysIleThrLys*****IleLysGlyLeuVal298
Db	820	ATCAGAAGGCCACCCAGATCAAGTCCCATCACCACCACTCCATCAAGGCTTCATC879
Qy	299	ValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAla318
Db	880	TTCGATACGTTCTCAGCAGGAGCTGACACATCTCTCAACCAACCCCTATGGGTGCTGGCG939
Qy	319	GluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValVal338
Db	940	GAGCTGATGAGGAACCCGCGATGTCGGCGAAAGCGCAGGCGAGGTGAGAGCGGCACCT999
Qy	339	GlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIle358
Db	1000	AAGGAGNAGACGACTGGGAGCTGGATGATGTCAGAGAGCTTAAGTACATGAATCGGTG1059
Qy	359	ValLysGluThrPheArgMetHisProProLeuProValValLysArgLysCys***Glu378
Db	1060	GTGAAGGAGACGATGAGGATGCACCTCCGATCCGCTTGATCCCGAGATCATGCAGAGAA1119
Qy	379	GluCys***IleAsnGly***Val***ProGluLysAlaLeu*****PheAsnValTyr398
Db	1120	GAATCGCTGTTAACCGGTTACGATTCCCGAACAAGCCGACAGATCATGATCAACAGCTCTGG1179
Qy	399	GlnValGly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPhe418

Db	1180	TCCATGGCGAGGAATCTCTCTACTGCGAAAAACCCGATACCTTTTCGCCCGCAAGGTTT	1239
QY	419	LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln	438
Db	1240	-----GACCAAGATTTCAAAGGATTTCATGGGAAATGATTTCGAG	1278
QY	439	LeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly	458
Db	1279	TTGCTCCCTCGTTCGGAGCGGAAGAATCTGCCCGGCTTGAACTTCGGGTCCGCAAC	1338
QY	459	**AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGln	478
Db	1339	GTTCAGATTCCATTCGGCGAGCTTCTTTACCACTTCGACTCGAAGTTG-----	1386
QY	479	GlyGlnIleLeuGlyGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThr	498
Db	1387	CGCGAAGGAATGAACCTTCTGAT-----ATGACATGTCTGAGCGCGAAGGCGCTTACC	1440
QY	499	ValProArgAlaHisSerLeuValCysValPro	509
Db	1441	GGAATACTAAGAACAAATCTTCTTCTGTCTCCC	1473
RESULT 14			
US-08-948-564-11			
: Sequence 11, Application US/08948564			
: Patent No. 6121512			
: GENERAL INFORMATION:			
: APPLICANT: Siminsky, Balazs			
: APPLICANT: Dewey, Ralph E.			
: APPLICANT: Corbin, Frederick T.			
: TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and			
: METHOD OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic P			
: NUMBER OF SEQUENCES: 23			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Virginia C. Bennett			
: STREET: PO Box 37428			
: CITY: Raleigh			
: STATE: No. 6121512th Carolina			
: COUNTRY: USA			
: ZIP: 27627			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.30			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/948,564			
: FILING DATE:			
: CLASSIFICATION: 800			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Bennett, Virginia C.			
: REGISTRATION NUMBER: 37,092			
: REFERENCE/DOCKET NUMBER: 5051-409			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 919-854-1400			
: TELEFAX: 919-854-1401			
: INFORMATION FOR SEQ ID NO: 11:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1657 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: single			
: TOPOLOGY: linear			
: MOLECULE TYPE: cDNA			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: 1..1548			
US-08-948-564-11			
Alignment Scores:			
Pred. No.:		3.57e-69	1657
Score:		590.00	150
Percent Similarity:		46.03%	Conservative: 99

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP44963/92
 FILING DATE: 02-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Perry, Lawrence S.
 REGISTRATION NUMBER: 31865
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-218-2100
 TELEFAX: 212-218-2200
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2174 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Eustoma russellianum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 92 to 1621
 IDENTIFICATION METHOD: by experiment
 US-08-606-505B-63

Alignment Scores:

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 Score: 582.50 Matches: 152
 Percent Similarity: 46.11% Conservative: 97
 Best Local Similarity: 28.15% Mismatches: 222
 Query Match: 24.31% Indels: 69
 DB: 3 Gaps: 13

US-09-857-581-66 (1-521) x US-08-606-505B-63 (1-2174)

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 DB 80 GACTTAAGCATGATGCTGTTGGAATGCGCTTTACTTCACATGCTGCATCATGATG 139
 QY 14 LeuPhe***HisLeuArgProThrPro***Ala***SerLysAlaLeuArgHisLeuPro 33
 DB 140 CTGTCTTCATGTCGAAACACTTGTGCAATATCTATGATGATATTCAGGCGGCCCGG 199
 QY 34 AsnProSerPro***ProArgLeuProPheLeuGlyHis***HisLeuLeuLysAsp 53
 DB 200 CTTCCACCTGGCCCGATA---GGGTGGCGGTCTCGGTGCGCTTCGCTTTTA---GGC 253
 QY 54 LysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer*** 73
 DB 254 ACATGCCTCATGTTGCATAGCTACATGATGCGCAAAATATGTCCTGTTATGTACTTA 313
 QY 74 ***PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeu 93
 DB 314 AAGGTAGGCAGCTGGTCTGCGCGTGGCATGCTGAGGTGCTAAGGCATTCCTC 373
 QY 94 Gln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***Leu 113
 DB 374 AAACACTTGAC---ATGAACTCTCGAATCGCGCCCTAATGCGGGCTACCCATTG 430
 QY 114 ThrTyrAsp***ValAla*****Pro***GlyProTyrTrp***PheValArg 132
 DB 431 GCCTATAATGTCAGGACATGCTGTTTGCAGACTATGTCCTCCAGATGGAAGCTGCTACT 490
 QY 133 LysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArg 152
 DB 491 AAACCTCAGCAATACATCTTCTGTTGGCAAGGCCCTGCGAGGCTGGGAAGAAGTTCCA 550
 QY 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
 DB 551 AGAAGAGACTGGGTATATGCTCTATGCAATGGCTGATCAGGCGGCACATGGCCAGCCA 610
 QY 173 LeuAsp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu 192
 DB 611 GTGGTGTGTCAGATGCTAATGCTATGCTATGCTGCAAGAACATGTTAGGCCAAGTGTGCTC 670

QY 193 -----GlyGluAlaGluGluLeuLeuArgAspIleAlaArg 203
 DB 671 AGCAAGCGACTTTTCGGGCTCTAAGGATCAGATCAATCAATGATCAAGATGTTGGTGGT 730
 QY 204 GluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys*** 223
 DB 731 GAGTTGATGACTGTTGCTGGCTATTTCACATAGGTGATTTATCCCTCGCATGTCATGG 790
 QY 224 LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
 DB 791 ATGATTTGCAGGGGATTCAGGCGGAATGAACAGGTTGCATAGAAGATTGATGTTG 850
 QY 244 ValGluArgValIleLysLysArgArg***IleValArgArgArg----- 258
 DB 851 TTGCTGCGTTTCTGGAAGAGACACACTGCATCGGCTCATGAGCGTAAGGACGCCCTGAT 910
 QY 259 -----AsnGlyGlu*****GluGlyGlu***SerGlyVal*** 272
 DB 911 TTCTTGAATTTTGTGCTTGCATGCAATGCGACAAATCTGAAGCGAA----- 955
 QY 273 LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*** 292
 DB 956 -----AGGCTTCAGACAGTC 970
 QY 293 ***IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla***** 312
 DB 971 AATATCAAGCGCTCTTTTATTGAACATGTTTACCGCTGGTACGATACATCTTCAACGCTC 1030
 QY 313 ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGlu 332
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 QY 333 Glu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeu 352
 DB 1091 GAAATGACGCGTGTGATGCGCGAGACGCGGCTTCTTGGACGACACATATCAAAAGTTG 1150
 QY 353 ProTyrIleArgAlaIleValLysGluThrPheArgMethHisProLeuProVal--- 371
 DB 1151 CCATATCTCCAGCCATCTCCAAAGAGCTTTCAGAAAGCATCTTCCAGCGCTTTAAAT 1210
 QY 372 ValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAla 391
 DB 1211 CTCACGAAATCGCGTCGCAAGCATGTGAAGTAATAGGACACATACATACCAAGGCACT 1270
 QY 392 Leu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSer 411
 DB 1271 AGGCTACGCTTACATATGGGCTATTGGAAGATCCATCTCTGTGGGAAATCCAAAT 1330
 QY 412 Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAsp 431
 DB 1331 GAATTTAACCTCATAGGTTTTTGAACGA-----AAGAATGCCAAGATCGAT 1378
 QY 432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly 451
 DB 1379 CCAGGAGGAATGATTTTGAGCTGATCCCATTTGGAGCTGGAAGAAGATTGCGCTGGA 1438
 QY 452 Val***LeuAlaThrSerGly***AlaThrLeuAlaSerLeuIleGlnCysPheAsp 471
 DB 1439 ACAAGATTGGGAATCTTCTAGTGGAGTATATTTTGGGAACCTTTGGTGCATCTTTTGT 1498
 QY 472 LeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMet 491
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 DB 1535 GATCAGCTTTTGGGCTTGTCTTCAGACAGCA-----GTGCGCTCTGCT 1579

Search completed: June 1, 2003, 01:49:12
 Job time : 97 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 01:40:43 ; Search time 237 seconds

(without alignments)
2964.128 Million cell updates/sec

Title: us-09-857-581-66.

Perfect score: 2396

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -LISTS=bits -START=1 -END=1 -MATRIX=blosum62
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Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	615.5	25.7	1554	9	US-09-938-842A-1009 Sequence 1009, Ap
2	593.5	24.8	1539	9	US-09-938-842A-199 Sequence 199, App
3	582.5	24.3	2174	10	US-09-814-786-63 Sequence 63, Appl
4	575.5	24.0	1927	10	US-09-814-786-64 Sequence 64, Appl

5	574.5	24.0	1824	10	US-09-814-786-11 Sequence 1, Appli
6	574	24.0	1575	9	US-09-938-842A-1997 Sequence 1997, Ap
7	568.5	23.7	1764	10	US-09-947-027-3 Sequence 3, Appli
8	568.5	23.7	1764	12	US-10-091-009-3 Sequence 1506, Ap
9	563.5	23.5	1563	9	US-09-938-842A-1506 Sequence 55, Appl
10	563	23.5	1545	9	US-10-142-231-55 Sequence 1, Appli
11	563	23.5	1933	9	US-10-067-534-1 Sequence 2124, Ap
12	559	23.3	1509	9	US-09-938-842A-2124 Sequence 72, Appl
13	556	23.2	1397	10	US-09-878-574-72 Sequence 2690, Ap
14	553	23.1	1491	9	US-09-938-842A-2690 Sequence 53, Appl
15	552	23.0	1539	9	US-10-142-231-53 Sequence 3, Appli
16	546.5	22.8	1883	10	US-09-796-256A-3 Sequence 2669, Ap
17	545.5	22.8	1557	9	US-09-938-842A-2669 Sequence 2172, Ap
18	531.5	22.2	1479	9	US-09-938-842A-2172 Sequence 1189, Ap
19	529	22.1	1488	9	US-09-938-842A-1189 Sequence 1, Appli
20	527	22.0	1929	9	US-09-899-643-1 Sequence 61, Appl
21	523.5	21.8	1503	9	US-09-938-842A-61 Sequence 2354, Ap
22	520.5	21.7	1506	9	US-09-938-842A-2354 Sequence 1301, Ap
23	516.5	21.6	1515	9	US-09-938-842A-1301 Sequence 2278, Ap
24	511.5	21.3	1494	9	US-09-938-842A-2278 Sequence 638, App
25	510	21.3	1512	9	US-09-938-842A-638 Sequence 655, App
26	505.5	21.1	1515	9	US-09-938-842A-655 Sequence 2477, Ap
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31	489	20.4	1509	9	US-09-938-842A-1499 Sequence 1473, Ap
32	488.5	20.4	1503	9	US-09-938-842A-1473 Sequence 1959, Ap
33	487	20.3	1557	9	US-09-938-842A-1959 Sequence 1382, Ap
34	479	20.0	1494	9	US-09-938-842A-1382 Sequence 1, Appli
35	475	19.8	1527	10	US-09-931-267-1 Sequence 3, Appli
36	475	19.8	1549	10	US-09-931-267-3 Sequence 814, App
37	473.5	19.8	1473	9	US-09-938-842A-814 Sequence 2, Appli
38	473	19.7	1527	10	US-09-931-267-2 Sequence 1, Appli
39	473	19.7	1708	10	US-09-796-256A-1 Sequence 835, App
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41	444	18.5	1990	10	US-09-349-385-9 Sequence 1300, Ap
42	433	18.1	1473	9	US-09-938-842A-1300 Sequence 2, Appli
43	429.5	17.9	1502	10	US-09-349-385-2 Sequence 795, App
44	428	17.9	806	10	US-09-770-445-795 Sequence 543, App
45	421.5	17.6	876	10	US-09-770-445-543

ALIGNMENTS

RESULT 1
US-09-938-842A-1009
: Sequence 1009, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: FILE REFERENCE: SAME, AND METHODS OF USE
: CURRENT APPLICATION NUMBER: US/09/938,842A
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1009
: LENGTH: 1554
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1009
Alignment Scores:


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Qy 52 LysAspLysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPhe 71
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Qy 498 ThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIleGly 514
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RESULT 3
US-09-814-786-63
; Sequence 63, Application US/09814786
; Patent No. US20020100072A1
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yasuhiro
; KIKUCHI, Shigeto
; SHIMADA, Yukihisa
; OHBAYASHI, Masaya
; SHIMADA, Ritsuko
; OKINAKA, Yatsushi
; ADDRESS: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 kb storage.
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS Ver3.30
; SOFTWARE: PATENT AID Ver1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/814,786
; FILING DATE: 23-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/616,990
; FILING DATE: 14-Jul-2000
; APPLICATION NUMBER: JP44963/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-218-2100
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RESULT 4
US-09-814-786-64
; Sequence 64, Application US/09814786
; Patent No. US20020100072A1
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yasuhiro
; KIKOKAWA, Shigeto
; SHIMADA, Yukihiisa
; OHBAYASHI, Masaya
; SHIMADA, Ritsuko
; OKINAKA, yasushi

TITLE OF INVENTION: NOVEL PLANT GENES
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112-3801

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.50 inch, 720 kb storage.
 COMPUTER: IBM PS/V
 OPERATING SYSTEM: MS-DOS Ver3.30
 SOFTWARE: PATENT AID Ver1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/814,786
 FILING DATE: 23-Mar-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/616,990
 FILING DATE: 14-Jul-2000
 APPLICATION NUMBER: JP44963/92
 FILING DATE: 02-MAR-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Perry, Lawrence S.
 REGISTRATION NUMBER: 31865

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-218-2100
 TELEFAX: 212-218-2200

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1927 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Campanula medium

FEATURE:
 NAME/KEY: CDS
 LOCATION: 180 to 1748
 IDENTIFICATION METHOD: by experiment
 SEQUENCE DESCRIPTION: SEQ ID NO: 64
 US-09-814-786-64

Alignment Scores:
 Pred. No.: 2,72e-74 Length: 1927
 Score: 575.50 Matches: 141
 Percent Similarity: 48.02% Conservative: 101
 Best Local Similarity: 27.98% Mismatches: 212
 Query Match: 24.02% Indels: 50
 DB: 10 Gaps: 11

US-09-857-581-66 (1-521) x US-09-814-786-64 (1-1927)

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 Qy 72 r*****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuph 92
 Db 401 CTTAAACTTGGTTCAAAGGGCACCGCTGCGCCCTCAAATCAAAGCGCCCGAGCGCTT 460
 Qy 92 eLeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg** 112
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 Qy 112 *LeuThrTyrAsp***-----ValAla*****Pro***GlyProTyrTrp***PheVa 131
 Db 518 CCTCGCGTAAATGCACAGACATGGTTTTTTCAGAAATATGCCCAAAATGGAAGCTTTT 577

Qy 131 lAtcLysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLe 151
 Db 578 CGGAAGCTATGTAGCTTGACATGTTAGGCCCGAAGGCACTCGAGGATGGGCTCATGT 637
 Qy 151 uArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***Ly 171
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 Qy 187 -----***SerMetMet** 191
 Db 758 AATCATACTCAGCGCGCCCTTTTGTATTATCAGGAGCAATTAGACTCGTCTCTTCTGC 817
 Qy 191 *LeuGlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGl 211
 Db 818 TTCTGCTTCTGTTAGTAGAATTCCAATATATGGTTATGGAGCTCATGAGGATGCGAGGTT 877
 Qy 211 uTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLy 231
 Db 878 GTTCATATTGGTGATTTTCATACCATATTTCATGATGATGATGATGATGATGATGATGAT 937
 Qy 231 sArgIleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysAr 251
 Db 938 TGATATGAAGTTATACAGAAAGATTGATGCTCTTTGTGAACAAATATGATCAAGGAACA 997
 Qy 251 gArg***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVa 271
 Db 998 TACAGATCCGCTCATGATCGCAAGATAATCTGTAT----- 1034
 Qy 271 l***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLy 291
 Db 1035 -TTTCTTGTATTTCTTATGGCGCTACCCAGAAACACACGCGGAGGATTCAGTCTAATCT 1093
 Qy 291 s*****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla** 311
 Db 1094 TGTAAATGTTAAGGCACCTCTTTTGATTTATTCACGCGGGGACGAGTACATCATCAAG 1153
 Qy 311 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaAr 331
 Db 1154 TGTATCGAATGGGCACTACCGGAAATGTTGAACCATCGACAGATCTAAACCGGGCCCA 1213
 Qy 331 gGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAs 351
 Db 1214 CGAAGAAATGGACCACTCATTCGAGAAACACAGAGACTAGAACATCTGCATACCAAA 1273
 Qy 351 nLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProVa 371
 Db 1274 CTTGCCATATTTCCAGCCCATATGCAAGAAACATTCGGAACACACCCITCCACGCCCTT 1333
 Qy 371 l---valLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGl 390
 Db 1334 AAACCTCCCAAGAAATCTCAACAGAACATCTGAAGTGGAGCGGATTCACATACCAAAA 1393
 Qy 390 yAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgPr 410
 Db 1394 CACTAGACTAATAGTAGAATATGGCAATAGGAGGAGCCCTAAAGTGTGGGAAATCC 1453
 Qy 410 oSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****Le 430
 Db 1454 ATTAGATTTTACTCCGGAAGCTTTCTTGAGTGAA-----AAACACCGCAAAAT 1501
 Qy 430 uAspLysArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysPr 450
 Db 1502 TGATCCCGAGGTAATCATTTTGAGTTAATCCCATTTTGGGCTGGACGAGGATATGTGC 1561
 Qy 450 oGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPh 470
 Db 1562 AGGGCTAGAAATGGGAGCGGCTCGTCCGAGTAGTACATATTAGGTACATTTGTGTGACCT 1621

QY 470 eAspLeuGlnValLeuGlyProGlnGlyGlnLeuLeuLysGly***AspAlaLysValse 490
 Db 1622 TGATTGGAATG-----CCTGAGGAGTTGTG-----GAAGTTAA 1657
 QY 490 rMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValprole 510
 Db 1658 TATGGAAGAGAGGTTTGGGATGCGATTGCAAAAAA-----GTGCTCT 1702
 QY 510 uAlaArgile 513
 Db 1703 TTCTGCTATT 1712

RESULT 5

US-09-814-786-1
 ; Sequence 1, Application US/09814786
 ; Patent No. US20020100072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIKUCHI, Yasuhiro
 ; KIKUCHI, Shigeto
 ; SHIMADA, Yukihisa
 ; OHBAYASHI, Masaya
 ; SHIMADA, Ritsuko
 ; OKINAKA, Yasushi
 ; TITLE OF INVENTION: NOVEL PLANT GENES
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112-3801
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
 ; COMPUTER: IBM PS/4
 ; OPERATING SYSTEM: MS-DOS Ver3.30
 ; SOFTWARE: PATENT AID Ver1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/814,786
 ; FILING DATE: 23-Mar-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/616,990
 ; FILING DATE: 14-Jul-2000
 ; APPLICATION NUMBER: JP44963/92
 ; FILING DATE: 02-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perry, Lawrence S.
 ; REGISTRATION NUMBER: 31865
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-218-2100
 ; TELEFAX: 212-218-2200
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1824 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Petunia hybrida
 ; STRAIN: Falcon Blue
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 116 to 1633
 ; IDENTIFICATION METHOD: by experiment
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-09-814-786-1

Alignment Scores:
 Pred. No.: 3,51e-74 Length: 1824
 Score: 574.50 Matches: 151
 Percent Similarity: 45.51% Conservative: 92
 Best Local Similarity: 28.28% Mismatches: 224

Query Match: 23.98% Indels: 67
 Db: 10 Gaps: 13
 US-09-857-581-66 (1-521) x US-09-814-786-1 (1-1824)
 QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***Val---LeuAlaLeuPhe***HisLeuArg 19
 Db 116 ATGATGCTACTTACTAGCTGTGTCAGCACTTCAATCTTTCTAATAGCACACATAATC 175
 QY 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro*** 39
 Db 176 ATTTCAACTCTTATTTCAAAACACTACCGCGCGCATCTACCG-----CCGGG 223
 QY 40 ProArg---LeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyr 58
 Db 224 CCAAGAGGGTGGCGCGGTGATCGGAGCACCTTCCACTTTTA---GGAGCCATGCCACATGT 280
 QY 59 Ala***IleAspLeuSerLysHisGlyProLeuPheSer*****PheGlySerMet 78
 Db 281 TCCTTAGCTAAATGGCAAAAAATATGGAGCAATCATGTATCTCAAGTTGGAACATGT 340
 QY 79 ProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAla 98
 Db 341 GGCATGGCAGTTGCTTCTACCCCTGATGCTGCTAAACATCTTGTAAACACATGTAT-- 397
 QY 99 ThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*** 117
 Db 398 ATCAACTTCTCCAATCGTCCACCTAATGCGAGTGCCACTCCTACTAGCTTATAATGCTCAA 457
 QY 118 **ValAla*****Pro***GlyProTyrTyr***PheValArgLysLeuIleMetAsn 137
 Db 458 GACATGGTTTTTGCACATTATGACCCAGCATGGAAGTTGCTAGGAATTAAGCAACTTG 517
 QY 138 AspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArg 157
 Db 518 CATATGCTAGGGGAAAGCCCTTAGAGATTGGCAATGCTGCGCAATGAGTAGGG 577
 QY 158 Lys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlu 177
 Db 578 CACATGCTAAATCAATGCTCGATATGATGCGAGGGCCAGAGGGTGTGGTGGCGGAG 637
 QY 178 GluLeuLysTyrTrp***AsnSerThr***SerMetMet***LeuGly----- 193
 Db 638 ATGTTGACATTGCGCATGGCCAAATATGATGCGACAGTGAATGCTAAGCAAAAGAGTATT 697
 QY 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle 208
 Db 698 GTAGATAAGGTGTTGAGGTAAATGAATTTAAGGACATGTTGTAGAGTTAATGACAATA 757
 QY 209 **GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLys 228
 Db 758 GCAGGTATTTCACATTGGTGAATTTATTCTCTGTTTGTAGCTTGGATGATTTACAAGGG 817
 QY 229 TyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValValGluArgValIle 248
 Db 818 ATAGAAAACGAATGAACCGTTTACATAAGAAGTTGATGCTTTATTGACAAAGATGTTT 877
 QY 249 LysLysArgArg***IleValArgArg----- 258
 Db 878 GATGACACAAAGCAACTACCTATGAACGTAAAGGGAAACACAGATTTCTGTGATGTTGT 937
 QY 259 ----**AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeu 277
 Db 938 ATGCAAAATGGGACAATCTGAAGAGAA----- 967
 QY 278 GluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeu 297
 Db 968 -----AGACTCAGTACCAACCAACATCAAGACATT 997
 QY 298 ValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeu 317
 Db 998 TTGCTGAATTTTCACAGCTGTGACGACACTTCTTCTAGTCAATAGATAATGGCACATT 1057

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QY 318 AlaGluLeuIleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerVal 337
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1058 GCAGAAATGATCAAGACCTCGCCATTTTGAAAGACGACACAGCAATGGATCAAGTC 1117

QY 338 ValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAla 357
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1118 ATTGAAGAAATAGCGCTTTACTCGAATCCGATATCCCAATCTCCCTTACTCCGAGCA 1177

QY 358 IleValLysGluThrPheArgMetHisProProLeuProVal---ValLysArgLysCys 376
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1178 ATTGCCAAGAAACATTTTCGAAACACCCCTCTACACCATTAATCTCTCTAGATCTCG 1237

QY 377 ***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsn 396
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1238 AACGAACCATGATAGTCGATGGTTATTACATACCAAAACACACTAGGCTTAGTGTAAAC 1297

QY 397 ValTppGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGlu 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1298 ATATGGCAANTGGAGAGATCCCAAGTTTGGGAATATCCACTAGATTAAATCCCGAA 1357

QY 417 ArgPheLeuGluThr***AlaGluGlyAla*****LeuAspLeuArgGly***His 436
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1358 AGATTCTTG-----AGTGAAGAAACTCCAAGATTGATCTCGAGGGAACGAT 1405

QY 437 PheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThr 456
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1406 TTGGAATTCATACCATTTGGTGCTGGACGAGAATTTGTGAGGAACAAAGATGGGAAT 1455

QY 457 SerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGly 476
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1466 GTAATGGTGAATATATATAGGAATTTGGTTCATTGTTGGAAT----- 1516

QY 477 ProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGly 496
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1517 -----TTACCAAGTGAAGATTATTGATTGATGATGGAAGAAAGCTTTTGGC 1561

QY 497 LeuThrValProArgAlaHisSerLeuValCysValProLeu 510
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1562 TTAGCTTTGCAGAAAGCT-----GTCCCTCTTT 1588
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RESULT 6

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US-09-938-842A-1997
; Sequence 1997, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1997
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1997
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Alignment Scores:

Pred. No.:	3,328-74	Length:	1575
Score:	574.00	Matches:	149
Percent Similarity:	47.41%	Conservative:	89
Best Local Similarity:	29.68%	Mismatches:	222
Query Match:	23.96%	Indels:	42

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DB: 9 Gaps: 13
US-09-857-581-66 (1-521) x US-09-938-842A-1997 (1-1575)

QY 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 TCCAAATCCAAAGACGACACCGTTGCTCGCTCCGGGACCTTGGCCA---CTTCGGATCGTC 183

QY 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 GGAACCTCCCGTCTCTAAACTCTGACGCTCTCCACACGCAATTCACAGCCCTAACCCCTA 243

QY 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 AAACATGGCCCTCTCATGAAGATCCACCTCGGTTCCAAACCTTCGATCGCTCTCTCC 303

QY 86 ProGluLeuPheLysPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 CCTGACATGGCTCGGAGGTCTCTCAAACCCACGACATCACT---TTCGCCAACCCACGAT 360

QY 106 GlnThrSerAla***Arg***LeuThrTyr---Asp*****ValAla*****Pro*** 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 CTCCTGAAGTCGAAAGATCAACACTTACGGTGGTGAACACATCTCTGGTCTCTCTTAC 420

QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 GGTACCCATTGAGGAGACTTCGTAAGCTCTGCGTCATGAAGATGTTCACTACCCCACT 480

QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 CTCGAAGCTTCTTACTCCACTCCCGGGAAGAACCCGACCAACCATTTGTCACATGTGCG 540

QY 165 Gln***AlaGluAla***LysProLeuAsp***ThrGlnGluLeu---LeuLysTrp*** 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 GAATAGCTCGTGAAGGATCACCAGTCAACCTCGGAGAGCAATATTTCTTCCATTTTC 600

QY 184 AsnSerThr***SerMetMet-----*****Leu 192
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 AAGCTCTGACAGAATGATGTGGGGCCCACTTTGAAGGACGACGAGAGACGACCTTA 660

QY 193 GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyr 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 GGA-----AACGAGCTCAAAACCCCTAATATCTGATATCTCCACATAGAAGGATTCAA 714

QY 213 SerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArg 232
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 715 AACTACTCAGATTTCTTCCGTTGTTCTCAAGATTTCGATTTCACAGGATGGTTAGCAG 774

QY 233 IleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg 252
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 775 ATGAAGGCCATGTGAAGAAGCTTGATCTCTTCTCGATAGAGTTATGGAGAGTCAAGTC 834

QY 253 ***IleValArgArgArg***AsnGlyGlu***GluGlyGlu***SerGlyVal*** 272
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 835 AAAATGGTG-----GGAAGAAAGCGGAGAGAGAAAGAAAT-----TTC 873

QY 273 LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*** 292
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 874 TTGCAATACTTACTAGA---GTTAAGATGATGATGAGAAGCTCTCTGTGTCATGACT 930

QY 293 ***IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla***** 312
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 931 CATGTCGAAGTCTCTCTCATGATGTTCTTGGTGTGTCGACACATCGGTAAACGCA 990

QY 313 ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGlu 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 991 TCCGAATTCGCATGCGCAGAGATTTGACGAGACCGGAGAGTGTAAACAGATCCGACTA 1050

QY 333 Glu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeu 352
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1051 GAACCTTCAACCAAGTTTGTGGCAAGACACATCGTTGAGGAATCACATTTACCTAAGCTT 1110

QY 353 ProTyrIleArgAlaIleValLysGluThrPheArgMetHisProLeuPro---Val 371
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Db 1111 CCTTACCTCAAGCGGTATGAAGAGACTCTTAGGCTTACCCCTACGCTTCCCTCTCTT 1170
QY 372 VALLYSARGLYSCYS**GluGluCys**IleAsnGly**Val**ProGluGlyAla 391
Db 1171 GTTCTCAGCAAAACAGCGAAACCTCGGCGGTGCGGATACACACTGTCCCTAAAGACTCC 1230
QY 392 Leu*****PheAsnValTrrpGlnValGly***Asp***LysTyrTrrpAspArgProSer 411
Db 1231 AAGATTTCATCAACGTTTGGCGGATTCATAGAGATCTCAGAAATGGGATGACCAAC 1290
QY 412 Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAsp 431
Db 1291 GAGTTCAAAACCTCAGAGGTTTGGAGAAAT-----TCGCTTGAT 1329
QY 432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly 451
Db 1330 TTCAATGGAGGATTTTAAAGTACTTGCTTTTGGGTGAGGAGAGATTTGCGCGG 1389
QY 452 Val***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAsp 471
Db 1390 ATTAACATGGCTCAGAGACTTGTCTGTCAACATTTGCTTCACTTCTTCACTTCTTTCAT 1449
QY 472 LeuGluValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMet 491
Db 1450 TCGAAA-----GCACCTCAGAGCAG-----AAGTTTGAGGTT 1482
QY 492 GluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAla 511
Db 1483 GAAGAGAAGTTGGTCTTCTTCTTAAGTTGAAGTCTCCACTGTGCTTCTTCTTCTTCCA 1542
QY 512 ArgIle 513
Db 1543 AGGTTG 1548

RESULT 7
US-09-947-027-3
; Sequence 3, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Lailong
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; FILE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: CAID5H
US-09-947-027-3

Alignment Scores:
Pred. No.: 2,57e-73 Length: 1764
Score: 588.50 Matches: 146
Percent Similarity: 46.14% Conservative: 87
Best Local Similarity: 28.91% Mismatches: 231
Query Match: 23.73% Indels: 41
DB: 10 Gaps: 13

US-09-857-581-66 (1-521) x US-09-947-027-3 (1-1764)

QY 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
Db 155 TCTCGCCTTCGCGGAAGATTGGCATATCCACCAGGCGCT---AAAGGGTTGCCACTTGTA 211
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QY 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Db 212 GGTAGCATGCACATGATG---GACCAATAACACACCGGTGGTAGCTAAACATAGTAAG 268
QY 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
Db 269 CAATATGGTGGCTCTTTTCATATGCGCATGGGTACTGTGCATATGTCATGTTTTCATCT 328
QY 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 329 CCTGAAATAGTCCCAAGTCTCGCAGTCCAGAC---AACATTTTCTCCACAGACCA 385
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----*****ValAla*****Pro*** 124
Db 386 GCCAACATAGCCATAACTTACTTAACTATGATCGTCAGATATGGCTTTGCCACTAC 445
QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
Db 446 GGTCTTTTCTGGCAGCAGATCGCTAAGCTCTGCTCAGTGAAGCTTTTACCCGAA--- 502
QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 503 -----ACGGCTGATCATGGAGTCTGTGACATGAGGTGGACTCAATGCIT 550
QY 165 Gln***AlaGluAla-----LysProLeuAsp***ThrGluGluLeuLeuLysTrp 182
Db 551 AAGACAGTTGAAGCCAATATAGCAGCCTGTGAATCTTGGGAATTGATTTTACGTTG 610
QY 183 ***AsnSerThr***SerMetMet***LeuGluGluAlaGluGluIleArgAsp----- 200
Db 611 ACCATGAACATCACTTACAGAGCAGCTTCGGGCTGATAAATAAGACAGGATGAGTTC 670
QY 201 -----IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle 218
Db 671 ATCAAGATTTTGCAGGAGTTCTCTAAGCTTTTGGAGCAITCAACATGCTGATTTTCAT 730
QY 219 **ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsn 238
Db 731 CCCTGGCTGGCTGGATTGACCCCAAGGCTCAGCGCTAGCTTGTCAAGGCTCGCAAG 790
QY 239 LysPheAspProValValGluArgValIleLysLysArg***IleValArgArgArg 258
Db 791 GCTCTTGATAGATTCATCGACTCTATCATCGATGATCAT-----ATCCAGAAAGAAAA 844
QY 259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlu 278
Db 845 CAGATAAGTTCTCTGAAGATGCTGAACCCGATATGTC-----GATGACATGCTAGCC 898
QY 279 Phe-----AlaGluAspGluThr***GluIleLys 288
Db 899 TTTTATGTTGAAGAACGAAAGTAGATGAATCAGATGATTTACAAAAGCCATCAGC 958
QY 289 IleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSer 308
Db 959 CTTACTAAAGACAACATCAAGGCCATATATCATGATGTGATTTGGTGGCAGCAGAGC 1018
QY 309 ThrAla*****ThrGluThrAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
Db 1019 GTGGCGTGGCAATAGACTGGTTCATGCGGAGCTATGAGACTCCAGAGGATCAAAA 1078
QY 329 ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
Db 1079 AGAGTCCAGCAAGAGCTCGCAGAGGTGGTGGTTAGAGCGCGCGCTGGAGAAAGTAT 1138
QY 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
Db 1139 ATTGACAAACTTACGTTCTTGAAATGCGCCCTCAACAAACCTTAGCATGCCACCACCA 1198
QY 369 LeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
Db 1199 ATCCACATCTCTTACATGAACACTCTCAGGATGCTGAGGTGCTGTTTATTTTCATCCA 1258
```


Qy	389	GLUGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp	408
Db	1259	AACCAACAAGGGTGATGATCAATTGCCTATTGGGAGACAGAATTTCATGGGA	1318
Qy	409	ArgProSerGlu***ArgProGluAArgPheLeuGluThr**AlaGluGlyGluAla***	428
Db	1319	GATCCTCATGCTTTTAAGCCCTTCAGAGTTTTGAACAGGGGTGCGT-----	1366
Qy	429	**LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met	448
Db	1367	-----GATTTAAAGGGAATCACTTTGACTTTATCCTTTCGGTCTGTCGGAGGTCT	1420
Qy	449	CysProGlyVal***LeuAlaThrSerGly**AlaThrLeuLeuAlaSerLeuLeuGln	468
Db	1421	TGCCCGGATGACAGCTTGGGTATACACACTTGATTTGGCTGTGCTCACTTGCTTCAT	1480
Qy	469	CysPheAspLeuGlnValLeuGlyProGlnGlyClnIleLeuLysGly***AspAlaLys	488
Db	1481	TGTTTACATGGGAATG-----CCUGATGGCATG-----AAACCGAGTGAA	1522
Qy	489	ValSerMetGluGlnArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal	508
Db	1523	CTTCACATGACTGATGATGTTGGACATCACCGGCCAACAGCACTGCATCGTTCGCGIT	1582
Qy	509	ProLeuAlaArgFile	513
Db	1583	CCGAGCAAGCGGTGTG	1597

RESULT 8

```

US-10-091-009-3
; Sequence 3, Application US/10091009
; Patent No. US2002013870A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
; TITLE OF INVENTION: COMPOSITION, AND
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Calcd5H
US-10-091-009-3

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US-09-857-581-66 (1-521) x US-10-091-009-3 (1-1764)

Qy 26 SerLysAlaLeuArdHisLeuProAsnProProSerPro***ProArgLeuProPhe145
 Db 155 TCTCGCTTCGCGAAGATGTCATATCCACAGGCT--AAAGGTTGCCACTGTGTA 211
 Qy 46 GlyHis***HisLeuLeuAspHisLeuHisTyAla***IleAspLeuSerLys 65
 Db 212 GTAGCATCCCATGATG--GACCAATACTCCAGTCGGTTAGCTAAACTAGTGAAG 268

QY 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
 Db 1319 GATCTGATGCTTTTAAAGCCTTCAAGTTTAAAGCAGGGTCCCT----- 1366
 QY 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
 Db 1367 -----GATTTTAAAGGAATACACTTTGAGTTTATTCCTTTTCGGGCTCTGGTCGAGGTCT 1420
 QY 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
 Db 1421 TCCTCCGGTATGACCTTGGGTATACACACTTGGTGGTGTGCTCATTGCTTCAT 1480
 QY 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
 Db 1481 TCTTTTACATGGGAATG-----CCTGATGGCATG-----AAACCGAGTGAA 1522
 QY 489 ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
 Db 1523 CTTCGATGACGTATGTTTGGACTCACCGCGCCCAAGCAACTCGACTCGTTGCCGTT 1582
 QY 509 ProLeuAlaArgIle 513
 Db 1583 CCGAGCAAGCGGTG 1597
 RESULT 9
 US-09-938-842A-1506
 ; Sequence 1506, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPT300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1506
 ; LENGTH: 1563
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1506
 Alignment Scores:
 Pred. No.: 1,17e-72 Length: 1563
 Score: 563.50 Matches: 146
 Percent Similarity: 45.45% Conservative: 94
 Best Local Similarity: 27.65% Mismatches: 241
 Query Match: 23.52% Indels: 47
 DB: 9 Gaps: 14
 US-09-857-581-66 (1-521) x US-09-938-842A-1506 (1-1563)
 QY 3 LeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro 22
 Db 55 CTTCGATCGTGTCTCTCTTTTCACTTCATCAGCTTCATCACACGGCGGGGAGGCGT 114
 QY 23 ***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeu 42
 Db 115 -----CCATATCTCCCGTCCACGA---GGTTGG 141
 QY 43 PropHeIleGlyHis***HisLeuLysAspLysLeuLeuHisLysAla***IleAsp 62
 Db 142 CCATCATAGGCAACATG---TTAATGATGGACCAACTCACCCACCGGTGTTTACCCAAAT 198

QY 63 LeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 82
 Db 199 TTACGTAAAGATGATGGGATGTCCCATCTCCCGCATGGATTCCTCCATATGACGCT 258
 QY 83 AlaSerThrProLysLeuPheLeuGln*****GluAlaThrSerPhe*** 102
 Db 259 GTCTCATCACCGAGTGGCTCGACAAGTCTTCAAGTCCAAAGACAGCCTC---TTCTCG 315
 QY 103 ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp---A*****ValAla*** 121
 Db 316 AACCGGCTCCACTATAGCTATAGCTATCTGACTTAGCAGCGGCGCATGGCTTTC 375
 QY 122 ***Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsn 141
 Db 376 GCTCACTACGACCGCTTTTGGACAGAGATGAGAAAAGTGTGTCTCAAGGTGTTTACG 435
 QY 142 AlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg 161
 Db 436 CGTAAAGACCTGAGTCATGGGCTTCAGTTCGT---GATGAGTGGACAAATGGTCCGG 492
 QY 162 ***MetaLaln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLys 181
 Db 493 TCGTCTCT-----TGTAACGTTGGTAAAGCTATAAAGCTCGGGAGCAAAATTTTGA 546
 QY 182 Trp***AsnSerThr***SerMetMet***LeuGlyGluAla-----Glu 196
 Db 547 CTGACCCCGCAACATACTTACCGGGGAGCGTTTGGGTCACTCGCAGGAGGACAGAC 606
 QY 197 GluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAsp 216
 Db 607 GAGTTCATAAGAACTTACAAAGAGTTCTCTAAGCTTTTGGAGCTTCAACGTAGCGAT 666
 QY 217 PheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
 Db 667 TTCAATCATTTCGGGTGCTCGATCCGCAAGGATTAACAGCGCTCTGTGAGGCG 726
 QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
 Db 727 CGTAATGATCTAGACGGATTTATTGAGATATTATCGATGAACAT-----ATGAAGAAG 780
 QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
 Db 781 AAGGAGAAATCAAAACGCTGTGGATGATGGGATGTTGTCGATACCGATATGTTGTATGAT 840
 QY 276 LeuLeuGluPheAlaGluAspGluThr----- 285
 Db 841 CTCTCTGCTTTTACAGTGAAGAGCCAAATTAGTCAGTGAGACGCGGATCTTCAAAAT 900
 QY 286 GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly 305
 Db 901 TCCATCAAACTTACCGGTGACAATATCAAGCAATCATCATGACGCTTATGTTGGAGGA 960
 QY 306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnPro*** 325
 Db 961 ACGGAACGCTAGCGTCGGCGATAGAGTGGCGCTTAACGAGGATTATACGACCCCGAG 1020
 QY 326 ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
 Db 1021 GATCTAAACCGGTCTCCAAAGAACTCGCCGAAGTCTGTGGACTTGACAGACGAGTTGAA 1080
 QY 346 GluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMet 365
 Db 1081 GAATCCGACATCGAAGAGTTGACTTATCTCAATGACACTCAAGNAACCTTAAGATG 1140
 QY 366 HisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly*** 385
 Db 1141 CACCCACGATCCCTCTCCCTCCAGAAACCGGAGGAGCACTAGTATCGACGCTTC 1200
 QY 386 Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***Lys 405
 Db 1201 TTCATTCCCAAGAAATCTCGTGATGATCAACCGCTTTCGCATAGACCGCACCCAC 1260
 QY 406 TyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGly 425

Db 1261 TCITGGACTACCGGACACGTTTAGACCATCGAGGTTTGTGAACCGGGCGTACCG--- 1317
Qy 426 GluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGly 445
Db 1318 -----GATTCAAGGGAGCAATTCGAGTTTATACGTTTCGGGTCGGGT 1362
Qy 446 Arg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSer 465
Db 1363 CGTAGATCGTCCCGGTATGCACTAGGTTTATACGCGCTTGACITAGCGGTCAT 1422
Qy 466 LeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnLeuLeuGlyGly*** 485
Db 1423 ATATTACATGCTTCACGTGGAATTA-----CCTGATGGGATG-----AAA 1464
Qy 486 AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeu 505
Db 1465 CCAAGTGAGCTGCACATGATGTGTTGGTCTCAGGCTCCTTAAAGCCACGCGCTT 1524
Qy 506 ValCysValProLeuAlaArgIle 513
Db 1525 TTCGCCGTGCCAACACCGCGCTC 1548

RESULT 10

US-10-142-231-55
; Sequence 55, Application US/10142231
; Publication No. US2003007796A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142,231
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-10-142-231-55

Alignment Scores:

Pred. No.: 1,36e-72 Length: 1545
Score: 563.00 Matches: 140
Percent Similarity: 47.99% Conservativity: 99
Best Local Similarity: 28.11% Mismatches: 211
Query Match: 23.50% Indels: 48
DB: 9 Gaps: 13

US-09-857-581-66 (1-521) x US-10-142-231-55 (1-1545)

Qy 33 ProAsnProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
Db 112 CCACAACTCCTTCA-----TGGCCCGTTATTGGGAATCTTCATCTCCTTACA 159
Qy 53 AspLysLeu---LeuHisTyrAla***TleAspLeuSerLysHisGlyProLeuPhe 71
Db 160 CAGAAAGTGCTATTCACCGAATCTATCTTCGCTTTCGGAGAGCTATGGACCAATCATG 219
Qy 72 Ser*****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeu 91
Db 220 CATCTTCAACTCGGCTCCGACAGCTTGGTTATTGCCCTTCAGATCTGGCCAAAGAA 279
Qy 92 PheLeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg 111
Db 280 TGCITCACACAATGAC---AAGCCCTTCGCTTCGCCACACGCTCTCTGCGAGGAAG 336
Qy 112 ***LeuThrTyrAsp*****Val---Ala*****Pro***GlyProTyrTrp***Phe 130
Db 337 CATGTAGGATATGACACAAAATCTCTAGTATGCTCCTTACGCTTCTCTACTGCGGAAC 396

Qy 131 ValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgPro 150
Db 397 CTTCCGAAATGTGCACGATCCAGATCTCTCTGCAACAGAAATGATCTCTCAGACAC 456
Qy 151 LeuArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGlu---Ala 169
Db 457 ATCCCGGTAGAGAAAGTTTCTGCTCTCATTCGTTGCTTGTGACAGTTGCCAGCGAGAG 516
Qy 170 ***LysProLeuAsp***ThrGluGluLeuLysTyr***AsnSerThr***SerMet 189
Db 517 GACACTCCAGTCAACATGAACGCGAGCTCTGATCTCAGCTTGTAGTATCATCTCCGT 576
Qy 190 Met***LeuGly-----GluAlaGlu 196
Db 577 ATGGTTGCCAACAAAGAAATATCAGGACGCTTTATCCGAGGAATAGGAGAGCGGAT 636
Qy 197 GluIleArgAspIleAlaArgGluValLeuLysIle***GlyLysSerLeuThrAsp 216
Db 637 CATTTTACCAGATGATAAACAGCTGTGTGTTCTTACTTGGAGCATTTGAGTTGGAGAT 696
Qy 217 PheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspIle 236
Db 697 TTCCTGCCCTTCTCAAGTGGCTTGATCTCAGGGTTTCATAGCTGCTATGAAAAAAGT 756
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 757 CAGCAGAAAGAGATGCTCTTTATGCAGAAATGGTGTGATGATCACCCTGAG---AAGAGA 813
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeu 276
Db 814 GGGAGAGTCGATCAAAATGCACAAGAC-----TTAATTGATGTTCTC 855
Qy 277 LeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLysGly 296
Db 856 ATCTCTGCACACACACCAATTCAGTCCGATAGTACGACAGATGTTGTGAAGCC 915
Qy 297 LeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluThrAla 316
Db 916 ACCGCCCTTACAATGCTGACGACGAGTACAGATACATCTCGTGACCATCATGGGCA 975
Qy 317 LeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSer 336
Db 976 TTGGCGGCTCTGATGACGACCCCTCATATTTTGACAAAGCCGACGAGCTGCACAG 1035
Qy 337 ValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArg 356
Db 1036 CATATCGGAGCGGCGGATTTAGAGAGAGAGATCTCCAGCAGCTGAAATATTGCGAG 1095
Qy 357 AlaIleValLysGluThrPheArgMetHisProProLeuPro---ValValLysArgLys 375
Db 1096 GCAATTGTGAAGAAACGTTGAGGCTATATCCAGCGGACCTCTCTTAGTTCTCTCAGCA 1155
Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Db 1156 GCCATTGAGATTGCACTGTTGAGGGTACCATGTCCTCCGAGGACCGCATGATTGTG 1215
Qy 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
Db 1216 AATGCTTGGCAATTCACAGACCGCGGAGTGTGGAAACGCGGACCGCTGTGATCTCT 1275
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
Db 1276 GAACGGTTTTGAAGAGCGGAAAGAG-----GTTGACCTAAAGGGCGG 1320
Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db 1321 GAGTTTGAATGATTCGTTTGGTTCAGGAGAGAATGTGTCGGGCGATGAGTCTGGCA 1380
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Db 1381 TTGAGTGTGTTTACGTATACGCTGGGAGGCTGCTCGAGAGTTCGAGTGTCTGT--- 1437
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495

Db 1438 ---CGAAGGTATGATA-----ATTGACATGACGGAAGTTG 1473
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
Db 1474 GGAATCAATGCCAAAGCA-----GTTCCGTTGGAGACATT 1512

RESULT 11

US-10-067-534-1

; Sequence 1, Application US/10067534
; Publication No. US20020187538A1
; GENERAL INFORMATION:
; APPLICANT: Essenberg, Margaret K.
; APPLICANT: Chen, Xiao-Ya
; APPLICANT: Luo, Ping
; APPLICANT: Wang, Yan-Hong
; TITLE OF INVENTION: cDNA Clone of (+)-Delta-Cadinene-8-Hydroxylase Gene from Cotton
; FILE REFERENCE: 006602-113
; CURRENT APPLICATION NUMBER: US/10/067,534
; CURRENT FILING DATE: 2002-02-07
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1933
; TYPE: DNA
; ORGANISM: Gossypium arboreum
US-10-067-534-1

Alignment Scores:

Pred. No.: 1,92e-72 Length: 1933
Score: 563.00 Matches: 154
Percent Similarity: 45.72% Conservative: 92
Best Local Similarity: 28.62% Mismatches: 234
Query Match: 23.50% Indels: 58
DB: 9 Gaps: 14

US-09-857-581-66 (1-521) x US-10-067-534-1 (1-1933)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeu----- 18
Db 154 ATGTTGTTCCCGAGTACCTGTTGTCATTTTGGTAGCCATATGGGAATTTCCATCTGGCAC 213
Qy 19 -----ArgProThrPro***Ala***SerLysAlaLeuArgHisLeuPro 33
Db 214 GTATGGACCATAGGAAGCCA-----AAGAAAGACATCGCCCAATTACCG 258
Qy 34 AsnProProSerPro***ProArg---LeuProPheIleGlyHis***HisLeuLeuLys 52
Db 259 -----CCGGGTCGCCGTGGTGGCAATAGTGGATATCTTCCATATCTTGA 306
Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 307 ACTGATAATCTTACCTTCGTGTTTACAGATTGGCTGCAGCTTACGGTCCCATCTACAG 366
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Db 367 CTTTGGCTAGGAACAATATTGCGTAGTATTAGCTCGGCACCACCTGCGCAACAGTG 426
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Db 427 GTTCGTGACACGACATCACA---TTTCTGAAAGGGATCTCCCGTTTGTGCAAGATT 483
Qy 113 LeuThrTyr-----Asp*****ValAla*****Pro***GlyProTyrTrp***Phe 130
Db 484 ATTACTTTGGCCTCAATGATATTGATTGTTTACAGTAGTCCAGATTGGAGATG 543
Qy 131 ValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrValAsn***LeuArgPro 150
Db 544 AAGAGAAAAGTCTGTGACGTCAATGCTTAGCCATAGTAGCATTAAGAGTTGTTATGGT 603
Qy 151 LeuArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla*** 170

Db 604 CTAAGAGGGAACAAGTGTCTTAAGCGGTACAAAATGTGCTCAA-----AGTCTGGC 657
Qy 171 LysProLeuAsp***ThrGlu---GluLeuLeuLysTrp***AsnSerThr***SerMet 189
Db 658 AAGCCAATTTGATTTGGTGAACGCGCATTTTAAACATCAATCAATCGATGATGACATG 717
Qy 190 Met***LeuGlyGluAla-----GluGluIleArg 199
Db 718 CTGTGGGTGGCAACAGAGGAGAGAGGGAAGGGCGGACGTTTGGGGCAATTTCGA 777
Qy 200 AspIleAlaArgGlnValLeuLysIle***GlyGlyTyrSerLeuThrAspPheIle*** 219
Db 778 GATCTCATAAACCGAATAATGCTGATCTGCAAAACCAACGTTTCTGATATTTCGCG 837
Qy 220 ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLys 239
Db 838 GTGCTTGCAGAGTTTGACATACAGGATGGGAAGAAATGACTAAATCGTTAAATCT 897
Qy 240 PheAspProValValGluArgValIleLysLysArg-----Arg***IleVal 255
Db 898 TTCGATAAGCTTTTCAACTCCATGATTGAAGAAAGAGAGAACTTTAGCAACAAATGAGC 957
Qy 256 ArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThr 275
Db 958 AAAGAAGATGGAACACACTGAAACAAAGAC-----TTCTTGACGTT 999
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys 295
Db 1000 CTGTGGACCTCAAGCAGAGAACGATACGGGAATATCGATAACATCAATCAAGTCAAG 1059
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Db 1060 GCCTGCTCATGACATTTGTCGGTGGAACTATACAACTCAACCAATGATGAATGG 1119
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Db 1120 ACAATGGCTGACTAATTCAMATCTCGAACAATGAAAGGTGAAGCAAGAATAGAC 1179
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
Db 1180 GATGTTGTCGGTTCGGATGGCGCGTCGATGAGACTCACTTCCTAAAGTGGCGTATCTA 1239
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Db 1240 GATGCTGCAGTAAAGAGAGACCTTCCGATTCACCCACCGATGCCACTCCTGTACCCGT 1299
Qy 376 Cys-----GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu***** 394
Db 1300 TGCCCGGGCGACTCAAGCAACGTTGGTGGCTATAGCGTACCAGAGGACCCAGGCTCTTC 1359
Qy 395 PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***Arg 414
Db 1360 TTAACATTTGGTGTATTAGAGGGATCCACAGCTTTGGGAAATCCTTTAGAATTCAG 1419
Qy 415 ProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly 434
Db 1420 CCGTAGAGGTTCTTGACT-----GATCATGAGAAGCTCGATTATTAGA 1464
Qy 435 ***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***Leu 454
Db 1465 AACGATTCGCGGTACATCGCGTTTGGTGGAGGAGAAATGTCGCCGAGTATCTCTC 1524
Qy 455 AlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 474
Db 1525 GTGCAAAAGATGTTGATTCTCTTGGCAGCAATGATCCATCTTATGATTGGAATTG 1584
Qy 475 LeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArg 494
Db 1585 GCGGACGCGTGAAGAAAATGACTTGAATGGCTTA----- 1617
Qy 495 AlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArg 512


```
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Syrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 72
LENGTH: 397
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LTB3028-056-Q1-B1-F1
US-09-878-574-72

Alignment Scores:
Pred. No.: 1,81e-72 Length: 397
Score: 556.00 Matches: 112
Percent Similarity: 84.8% Conservative: 0
Best Local Similarity: 84.8% Mismatches: 20
Query Match: 0 Indels: 0
DB: 10 Gaps: 0

US-09-857-581-66 (1-521) x US-09-878-574-72 (1-397)
QY 266 GlyGlu***SerGlyVal**LeuAspThrLeuLeuGluPheAlaGluAspGluThr*** 285
DB 1 GGTGAGGTCACGGGGGTTTCTTGACACTTGTCTGTAATTCGTTGAGTTCGTTGAGGATGACACCATG 60
QY 286 GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly 305
DB 61 GAGATCAAAATCACCAGGACCATCAAGGGTCTTGTGTGCGACTTTTCTCGCAGGA 120
QY 306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro*** 325
DB 121 ACAGACTCCACAGCGGTGCACAGAGTGGGATGGGATGGGACACTATCAACAACTCCTAAG 180
QY 326 ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
DB 181 GTGTTGAAAGGCTCGTGAGAGGTCTACAGTGTGTGTGGGAAAGGACAGACTTGTGGAC 240
QY 346 GluValAspThrGluAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMet 365
DB 241 GAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAGGAGACATTCGCGATG 300
QY 366 HisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly*** 385
DB 301 CACCGCCACTCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGTGAGATTAATGGATAT 360
QY 386 Val***ProGluGlyAlaLeu*****PheAsnVal 397
DB 361 GTGATCCAGAGGGAGCATTTGATCTCTTCAATGTA 396

RESULT 14
US-09-938-842A-2690
Sequence 2690, Application US/09938842A
Patent No. US20030160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2690
LENGTH: 1491
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2690

Alignment Scores:
Pred. No.: 3,85e-71 Length: 1491
Score: 553.00 Matches: 142
Percent Similarity: 50.20% Conservative: 103
Best Local Similarity: 29.10% Mismatches: 205
Query Match: 23.08% Indels: 38
DB: 9 Gaps: 16

US-09-857-581-66 (1-521) x US-09-938-842A-2690 (1-1491)
QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 90 CCACCCGGACCC---CCAGACTTCCTATAATTTGGAACCTTCACCAACTGATGATCAAA 146
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
DB 147 ---CCTCATCGTTTCGATGTTCAAAATATCCGAACATATGGACCTTAATATGCCCTAAAG 203
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
DB 204 TTTGGAGCGGTGCTACTGTGTGGCATCTACACAGACAGACAGTGTAGGAAGTCTTAA 263
QY 95 *****GluAlaThrSerPhe***ThrArgPheGluThrSerAla***Arg***LeuThr 114
DB 264 ACATTTGACGTAGTAATGTTGTCGCCACCAAAATATGACCTATATCCCGCAAGA---GTTAGC 320
QY 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 321 TACATTTAAAGATCTATGCTTTTCTCTATAGCAATATTTGGAGGAGGTACCAAGAA 380
QY 134 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 381 ATCAGAGTTCTTGAACCTCTACACCGCAAAAGGTCGAATCATTTCAACATACAGA 440
QY 154 GluGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 441 GAAGAAGTTCCAGCCCTCGTTGATTTCATCAACAAGCTGCTTCATTGGAGAAACCGATT 500
QY 174 Asp***ThrGluGluLeuLeuLysTyrP***AsnSerThr***SerMetMet***LeuGly 193
DB 501 AACTTGAACAAGAAGTTAATGAACATATCAGGAAGTGTGATTGTAGAGTTGTCATTGCT 560
QY 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeu----- 206
DB 561 ATCAATCTTCAGGAAGTAACTTGAACATCTATTAAGCATCCTACAGATGAGATTAAAGAT 620
QY 207 LysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysVal 226
DB 621 GAGTTGGTGGGAGTTTTCAGCAGCAGCAGATTACTTT---CCGGTT-----GTT 665
QY 227 GlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAspProValValGluArg 246
DB 666 GGTAGATCATCGATGAGTACAGGGTTCATAGCAAAATGTGAGAGCTTTTTCAGGCA 725
QY 247 ValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu*****GluGly 266
DB 726 ATGATGTCATTTTTCATCAATCTATAAGCATCCTACAGATGAGATTATTAAGAT 785
QY 267 Glu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***** 285
DB 786 GAT-----ATAATTGACTTCTCTCAAGATGAAAGGGGAGAGACTACTACTT 833
```

QY		286	--GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAla	304
Db		834	GGGAGTTTCACCTTACTCCGCACCACCAAGAATCTTGAGAAATATTCTCAACGCT	893
QY		305	Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro	324
Db		894	GGAAATAGACACTTCTGCACAAGTATTGACATGGGTGATGACATATTGTATTCAAACCCA	953
QY		325	**ValLeu*****AlaArgGluGlu**TyTyrSerValVal---GlyLysAsp***Leu	343
Db		954	AGAGTTTGAAGAACGCCGCGGAGGTGAGACAGTGTATAAACAACAAGAATGATATC	1013
QY		344	ValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPhe	363
Db		1014	ATAGAAGAA---GATATAGAACGACTCCAATATCTGAAAAATGCTAATTAAGAAGACGTTT	1070
QY		364	ArgMetHisProLeuPro---ValValLysArgLysCys**GluGluCys***Ile	382
Db		1071	AGATAAACCCACTTGTGCCACTTCATAATCCAAGAGAGGCTTCAAAAGAATGATAAGATC	1130
QY		383	AsnGly***Val**ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***	402
Db		1131	GGAGGTATATATATCCAAAGAAAACATGGATCCATGTTAATATATGGGTATTCATAGG	1190
QY		403	Asp***LysTyrTrpAspArgProSerGlu**ArqProGluArgPheLeuGluThr***	422
Db		1191	AATCCAAACGTTTGGAAAGATCCAGAAGCTTCATTCGCCAGAGGTTTATGGATAGC---	1247
QY		423	AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProphe	442
Db		1248	-----CAGATTGACTATAAAGGGTTGAACCTTGAGTTTGTGTTCGCGTTT	1289
QY		443	GlySerGlyArg***MetCysProGlyVal**LeuAlaThrSerGly***AlaThrLeu	462
Db		1290	GTTAGCGGAGGAGCATATGCCCTGGTATTGGAAATGGGTATGGCTTGGTTCCTGACT	1349
QY		463	LeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeu	482
Db		1350	CTTATCAATCTCTTTATTCGATTTCGATTGGAAGCTT-----CCAGAAGGAATGAAGGTA	1403
QY		483	Lysely***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAla	502
Db		1404	-----GCAGATGTTGATCTTCAGASATCATATGCAGCTTGTTCCTCAAGAAA	1451
QY		503	HisSerLeuValCysValProLeu	510
Db		1452	ATCCCACTTCAGGTTATCCGGGTC	1475

RESULT 15

```

US-10-142-231-53
; Sequence 53, Application US/10142231
; Publication NO. US2003007796A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142.231
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Taxus cuspidata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1539)
; OTHER INFORMATION: "n" equals any oligonucleotide
US-10-142-231-53

```

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Alignment Scores:
Pred. No.: 5,686-71 Length: 1539
Score: 552.00 Matches: 136
Percent Similarity: 48.80% Conservative: 104
Best Local Similarity: 27.20% Mismatches: 214
Query Match: 23.04% Indels: 42
DB: 9 Gaps: 13

US-09-857-581-66 (1-521) x US-10-142-231-53 (1-1539)

QY 29 LeuArgHisLeuProAsn-----ProSerPro***ProArgLeuPro 43
||||| ||| ||| ||||| ||| ||| ||| |||
Db 106 CTCGCGCGCTGGAACAATCGAAGAAGATGCCGCCGCCCAATCCA---TGGCGC 162
QY 44 PheIleGlyHis**HisLeuLeuLysAspLysLeuHisTyra***IleAspLeu 63
|||||: ||| ||| ||||| :|
Db 163 ATCGTGGGAATCTCCACCACTG--GGAAGCTTCCCAACCGTAATCTGGAAGAGCTC 219
QY 64 SerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAla 83
||||| ||| ||| ||||| ||| ||||| ||| ||||| |||
Db 220 GCAAGAACAACGGACCCCATCATGCTATGAATGGTGGTTCCTGCTGCCGCTATCGTT 279
QY 84 SerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe**Thr 103
||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :|||
Db 280 TCTTCTCTGCCATCGCAAAAGATTGTGAAAACTCATGATCTGGT---TTGGCAGC 336
QY 104 ArgPheGlnThrSerAla***Arg**LeuThrTyraSp-----ValAla***** 122
||||| ||||| ||||| ||| :||| ||||| :||| ||||| :||| ||||| :|||
Db 337 CACCGCGAAGCGCCGAGAAATACATACGCTATTAATTACAGGATATAGTTTCTCT 396
QY 123 Pro***GlyProTyTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAla 142
||||| ||||| ||||| ||||| ||||| :||| ||||| ||||| ||||| |||||
Db 397 COCTACGGACCTTACTGCGAGACAGATGAAGAAATATCGCTGGTGAATGTTGAATGCC 456
QY 143 ThrThrValAsn**LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg** 162
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 AGAAGATCGACTCGTGTGAGATCCGTAGAGAGAGAGAGTGTCTGTTATATCTGTCG 516
QY 163 Met-----AlaGln***AlaGluAla***LysProLeuAsp*** 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 517 GTGTGGGAGAAGACGACGAGGTGCGTCCGCTCAATCTGAGCAAGACGCTGTCTATCC 576
QY 176 ---ThrGluGluLeuLeuLysTrp***AsnSerThr**SerMetMet***LeuGlyGlu 194
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 577 CTTCACAGGACTCATGTTGCAGATCTTTCAGTAACGATACGCGGGGATACGAC 636
QY 195 AlaGluGluIleArgAspIleAlaArgValLeuLysIle***GlyIuTyrSerLeu 214
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 637 GTCACCGCCATTAAAGAAATGATGCGAGGTGTCTGAGACGCGGGAGGCTTTTAACAT 696
QY 215 ThrAspPheIle***ProLeuLys**LeuLysValGlyLysTyrgLysArgIleAsp 234
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 GGAGATTATTTCCATGGATGACTGGATGATTTCGAGGTATACAGCGGCCATGACG 756
QY 235 AspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***Ile 254
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 757 AAGGCACAGATTATTTCCGACAGTCTATACGAAAATTTATAGCAACACCCAG-- 810
QY 255 ValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal**LeuAsp 274
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 811 ---AGGACGAGACCATGGAGACACTCAACACCAAAAGAC-----ATAATTGAC 858
QY 275 ThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile 294
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 859 GCCCTGTTCCAGATG-----GAGAACACCGATGGCTCCACCTACCAATGGAATAATC 912
QY 295 LysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGlu 314
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 913 AAGCCGCTGCTTTTGGGTATTTTCTGGCGGACGGAGACGAGCTCCACTGCTGGA 972
QY 315 TrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu*** 334
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 973 TGGCGCATGAGCGCATGCTTTGAAACCCCTGAGTGGCCGAGAAAGCTGCAAGAAAGATC 1033

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 16:59:35 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: us-09-857-581-66
Perfect score: 2396
Sequence: 1 MLELALGLXVLALFXHLRP.....ARSLVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues
Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2396	100.0	521	1	US-09-857-581-2
2	2396	100.0	521	1	US-09-857-581-26
3	2396	100.0	521	1	US-09-857-581-28
4	2396	100.0	521	1	US-09-857-581-30
5	2396	100.0	521	1	US-09-857-581-32
6	2396	100.0	521	1	US-09-857-581-34
7	2396	100.0	521	1	US-09-857-581-36
8	2396	100.0	521	1	US-09-857-581-24
9	2304	96.2	499	1	US-09-857-581-16
10	2304	96.2	499	1	US-09-857-581-18
11	2304	96.2	499	1	US-09-857-581-20
12	2304	96.2	499	1	US-09-857-581-22
13	2304	96.2	499	1	US-09-857-581-40
14	2304	96.2	499	1	US-09-857-581-48
15	2304	96.2	499	1	US-09-857-581-55
16	2304	96.2	499	1	US-09-857-581-57
17	2304	96.2	499	1	US-09-857-581-59
18	2298	95.9	498	1	US-09-857-581-38
19	2293	95.7	498	1	US-09-857-581-61

ALIGNMENTS

RESULT 1
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
; US-09-857-581-2

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALFXHLRPPTXAKSKALRHLPPNPSPXPRLPFIHGHLLKDKLLHYAX 60
Db 1 MLELALGLFVLALFLHRLPTPSAKSKALRHLPPNPSPKPRLPFIHGHLLKDKLLHYAL 60
QY 61 IDLSKKGHPFSLSGSMPTVASTPELPKLFLOXHEATSFXTFTQTSAXRXLTYDXVA 120
Db 61 IDLSKKGHPFSLSGSMPTVASTPELPKLFLOXHEATSFXTFTQTSAXRXLTYDXVA 120
QY 121 XXPGPYWKFVYRKLIMNDLLNATVVKLRPLRTOQIRKLRVMAQSAEAKPLDXTBELL 180
Db 121 MYPGPGYWKVYRKLIMNDLLNATVVKLRPLRTOQIRKLRVMAQSAEAKPLDXTBELL 180
QY 181 KWNSTXSMXKLGEABEIRDIAREVLKIXGYSITDFIXPLKLVKGVKXRIIDILNKF 240
Db 181 KWNSTISMMVLGEABEIRDIAREVLKIFGYSITDFIWPPLKLVKGVKXRIIDILNKF 240
QY 241 DPVVERVTKRDXIVRRKXGEXYEGXSVXLTLLFAEDTXXEIKITKXIKGLVVD 300
Db 241 DPVVERVTKRDXIVRRKXGEXYEGXSVXLTLLFAEDTXXEIKITKXIKGLVVD 300
QY 301 XFSAGXDSTAXTETWALAEELNNPKVLXAXAREEYXSVVGKDXLVDVDTQNLPIRAIVK 360
Db 301 FFSAGTDSATATWALAEELNNPRVLQKAREEYXSVVGKDXLVDVDTQNLPIRAIVK 360
QY 361 ETPRHHPLPVVKKCBECXINGVXVPEGALXAFNVMQVGDXXKYWDRSEKPEPFLE 420
Db 361 ETPRHHPLPVVKKCBECXINGVXVPEGALVFNVMQVGRDPKYWDRSEKPEPFLE 420
QY 421 TXAEGEAXLDRGXHFOLLFFGSGRXCPCGXVLTATGXATLLASLIQCPLQVLGPQGQ 480
Db 421 TGAEGEAGPLDRGHFOLLFFGSGRRMCPGVNLTATGMATLLASLIQCPLQVLGPQGQ 480
QY 481 ILKGDAXVMEERAGLTVPPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGDAXVMEERAGLTVPPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26


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Db 121 MYPFGYKFKVRLINNDLLNATTNNKLRPLTQOIRKFLRVVAQGAQKPLDTEELL 180
Qy 181 KXNSTYXMMXGAEAEIRDIAREVLKIXGEYSLTDPIPLKXKLVKGYEKRIDDIILNF 240
Db 181 KWTNSTISMMMLGAEAEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDIILNF 240
Qy 241 DPVVERVIKRRXIVRRRNGEXXGEGXGVKLDTLLEFAEDSTXEIKITKXIKGLVVD 300
Db 241 DPVVERVIKRRIVRRRNGEVEGEVGVFLDTLLEFAEDSTXEIKITKDHIGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVXXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPPLPVVRKCKEEXINGXVPEGALXXFNWQVGVXGXKXKXWDRPSEKRPERFLE 420
Db 361 ETRFMHPPPLPVVRKCKTECEINGYVPEGALILFNWQVGRDPKYWDRPSEKRPERFLE 420
Qy 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPCGVKXATLASLIQCDFDLQVLGPQQ 480
Db 421 TXAEGEAXXLDLRCQHFQLLPFGSGRMCPCGVNLTSGMATLASLIQCDFDLQVLGPQQ 480
Qy 481 ILKGXDAKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521

RESULT 5
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLVIALFHLRPTTAXSKALRHLNPPSPXPRLPFIQHXHLLKDLHYAX 60
Db 1 MLELALGLVIALFHLRPTTAXSKALRHLNPPSPKPRLPFIQHLHLLKDLHYAL 60
Qy 61 IDLSKKGHPLFSXPGSMPTVASTPELFLKLOXXEATSFXTRFOTSAKXRLTYDXVA 120
Db 61 IDLSKKGHPLFSXPGSMPTVASTPELFLKLOTHEATSFNTFOTSAIRRLTYDSSVA 120
Qy 121 XXPGPYKXVVRKLIIMNDLLNATTNNKLRPLRTOQIRKXLRXMAQAEAKPLDXTBELL 180
Db 121 MYPFGYKFKVRLINNDLLNATTNNKLRPLRTOQIRKFLRVVAQGAQKPLDTEELL 180
Qy 181 KXNSTYXMMXGAEAEIRDIAREVLKIXGEYSLTDPIPLKXKLVKGYEKRIDDIILNF 240
Db 181 KWTNSTISMMMLGAEAEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDIILNF 240
Qy 241 DPVVERVIKRRXIVRRRNGEXXGEGXGVKLDTLLEFAEDSTXEIKITKXIKGLVVD 300
Db 241 DPVVERVIKRRIVRRRNGEVEGEVGVFLDTLLEFAEDSTXEIKITKDHIGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVXXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPPLPVVRKCKEEXINGXVPEGALXXFNWQVGVXGXKXKXWDRPSEKRPERFLE 420
Db 361 ETRFMHPPPLPVVRKCKTECEINGYVPEGALILFNWQVGRDPKYWDRPSEKRPERFLE 420

RESULT 6
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLVIALFHLRPTTAXSKALRHLNPPSPXPRLPFIQHXHLLKDLHYAX 60
Db 1 MLELALGLVIALFHLRPTTAXSKALRHLNPPSPKPRLPFIQHLHLLKDLHYAL 60
Qy 61 IDLSKKGHPLFSXPGSMPTVASTPELFLKLOXXEATSFXTRFOTSAKXRLTYDXVA 120
Db 61 IDLSKKGHPLFSXPGSMPTVASTPELFLKLOTHEATSFNTFOTSAIRRLTYDSSVA 120
Qy 121 XXPGPYKXVVRKLIIMNDLLNATTNNKLRPLRTOQIRKXLRXMAQAEAKPLDXTBELL 180
Db 121 MYPFGYKFKVRLINNDLLNATTNNKLRPLRTOQIRKFLRVVAQGAQKPLDTEELL 180
Qy 181 KXNSTYXMMXGAEAEIRDIAREVLKIXGEYSLTDPIPLKXKLVKGYEKRIDDIILNF 240
Db 181 KWTNSTISMMMLGAEAEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDIILNF 240
Qy 241 DPVVERVIKRRXIVRRRNGEXXGEGXGVKLDTLLEFAEDSTXEIKITKXIKGLVVD 300
Db 241 DPVVERVIKRRIVRRRNGEVEGEVGVFLDTLLEFAEDSTXEIKITKDHIGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVXXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPPLPVVRKCKEEXINGXVPEGALXXFNWQVGVXGXKXKXWDRPSEKRPERFLE 420
Db 361 ETRFMHPPPLPVVRKCKTECEINGYVPEGALILFNWQVGRDPKYWDRPSEKRPERFLE 420
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Qy 421 TXAEGEAXXLDLRCGHFQQLPFGSGRMCPGVXLTATSGXATLLASLIQCFDQLVLPQGO 480
Db 421 TGAGEARPLDRCGHFQQLPFGSGRMCPGVNLTATSGMATLLASLIQCFDQLVLPQGO 480
Qy 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521
RESULT 7
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36
Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLELALGLVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHLLKDLKLLHYAX 60
Db 1 MLELALGLVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHLLKDLKLLHYAL 60
Qy 61 IDLSKHGFLFSXFGSMPTVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVA 120
Db 61 IDLSKHGFLFSXFGSMPTVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVA 120
Qy 121 XXPXGPMXKXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 300
Db 121 XXPXGPMXKXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 300
Qy 241 DPVVERVVKRRXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 360
Db 241 DPVVERVVKRRXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 360
Qy 301 XFSAGXDSATXATEWALAEELNPPVLAAXAREEYVGVKDLVDEVDTONLPYIRAIK 420
Db 301 XFSAGXDSATXATEWALAEELNPPVLAAXAREEYVGVKDLVDEVDTONLPYIRAIK 420
Qy 361 ETRFMHPPPLPVVKRCXBECEINGVYVPEGALVFNVMQVGVXDXKYWRPSEPRERFLE 480
Db 361 ETRFMHPPPLPVVKRCXBECEINGVYVPEGALVFNVMQVGVXDXKYWRPSEPRERFLE 480
Qy 421 TXAEGEAXXLDLRCGHFQQLPFGSGRMCPGVXLTATSGXATLLASLIQCFDQLVLPQGO 480
Db 421 TGAGEARPLDRCGHFQQLPFGSGRMCPGVNLTATSGMATLLASLIQCFDQLVLPQGO 480
Qy 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521

RESULT 8
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24
Query Match 100.0%; Score 2396; DB 1; Length 522;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLELALGLVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHLLKDLKLLHYAX 60
Db 1 MLELALGLVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHLLKDLKLLHYAL 60
Qy 61 IDLSKHGFLFSXFGSMPTVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVA 120
Db 61 IDLSKHGFLFSXFGSMPTVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVA 120
Qy 121 XXPXGPMXKXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 180
Db 121 XXPXGPMXKXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 180
Qy 181 KXNXTXSMXKLGEAEERDIAREVLIKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
Db 181 KXNXTXSMXKLGEAEERDIAREVLIKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
Qy 241 DPVVERVVKRRXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 300
Db 241 DPVVERVVKRRXIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXIKGLVVD 300
Qy 301 XFSAGXDSATXATEWALAEELNPPVLAAXAREEYVGVKDLVDEVDTONLPYIRAIK 360
Db 301 XFSAGXDSATXATEWALAEELNPPVLAAXAREEYVGVKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPPLPVVKRCXBECEINGVYVPEGALVFNVMQVGVXDXKYWRPSEPRERFLE 420
Db 361 ETRFMHPPPLPVVKRCXBECEINGVYVPEGALVFNVMQVGVXDXKYWRPSEPRERFLE 420
Qy 421 TXAEGEAXXLDLRCGHFQQLPFGSGRMCPGVXLTATSGXATLLASLIQCFDQLVLPQGO 480
Db 421 TGAGEARPLDRCGHFQQLPFGSGRMCPGVNLTATSGMATLLASLIQCFDQLVLPQGO 480
Qy 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVPRASHLVCPVLARIGVASKILLS 521
RESULT 9
US-09-857-581-16
; Sequence 16, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581

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; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
; US-09-857-581-16

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAKSKALRHLNPPSPXPRLPFFIGHXHLKDKLLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTSAKSKALRHLNPPSPXPRLPFFIGHLHLKDKLLHYALIDLKSKHGPLFSLS 60

QY 75 FGSMTVVAASPPELFLQXEAATSFTRFQTSAXRLTYDXXVAXXPXGPMYXVVRKL 134
DB 61 FGSMTVVAASPPELFLQTHEATSFTRFQTSAXRLTYDLSVAMVFFGPMYXVVRKL 120

QY 135 IMNDLLNATTNKLRLPTQIRKRLXMAQAEAKPLDXTTELLKXNXTSXMMMLGE 194
DB 121 IMNDLLNATTNKLRLPTQIRKRLVMAQAEAKPLDXTTELLKXNXTSXMMMLGE 180

QY 195 ABEIRDIAREVLKXGEYSLTDIFXPLKXKLVGYEKRIDDLNKFDPVVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLTDIFWPLKXKLVGYEKRIDDLNKFDPVVERVVKRREI 240

QY 255 VRRXNGEXXGEXSGVLDLTLLEFAEDTBEIKITKXIKGLVVDXFSAGXDSTAXTE 314
DB 241 VRRXNGEVVEGEVSGVLDLTLLEFAEDTBEIKITKXIKGLVVDXFSAGIDSTAVATE 300

QY 315 WALAELINNPVXKXAREEYSVVGKDLVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 374
DB 301 WALAELINNPVQKAREEYSVVGKDLVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 360

QY 375 KCXEECXINGXVPEGALXXFNVMQVGDXYKWDPSERPERFLETXAEGEAXXLDLRG 434
DB 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWDPSERPERFLETGAEGEARFDLRG 420

QY 435 XHFQLLPFGSGRXCWPCGVXKATLSGXTLLASLIQCFDLQVLGPOGQILKGDADKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKYSMEER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-18
; Sequence 18, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
; US-09-857-581-20

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Vicia villosa
; US-09-857-581-18

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAKSKALRHLNPPSPXPRLPFFIGHXHLKDKLLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTSAKSKALRHLNPPSPXPRLPFFIGHLHLKDKLLHYALIDLKSKHGPLFSLS 60

QY 75 FGSMTVVAASPPELFLQXEAATSFTRFQTSAXRLTYDXXVAXXPXGPMYXVVRKL 134
DB 61 FGSMTVVAASPPELFLQTHEATSFTRFQTSAXRLTYDLSVAMVFFGPMYXVVRKL 120

QY 135 IMNDLLNATTNKLRLPTQIRKRLXMAQAEAKPLDXTTELLKXNXTSXMMMLGE 194
DB 121 IMNDLLNATTNKLRLPTQIRKRLVMAQAEAKPLDXTTELLKXNXTSXMMMLGE 180

QY 195 ABEIRDIAREVLKXGEYSLTDIFXPLKXKLVGYEKRIDDLNKFDPVVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLTDIFWPLKXKLVGYEKRIDDLNKFDPVVERVVKRREI 240

QY 255 VRRXNGEXXGEXSGVLDLTLLEFAEDTBEIKITKXIKGLVVDXFSAGXDSTAXTE 314
DB 241 VRRXNGEVVEGEVSGVLDLTLLEFAEDTBEIKITKXIKGLVVDXFSAGIDSTAVATE 300

QY 315 WALAELINNPVXKXAREEYSVVGKDLVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 374
DB 301 WALAELINNPVQKAREEYSVVGKDLVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 360

QY 375 KCXEECXINGXVPEGALXXFNVMQVGDXYKWDPSERPERFLETXAEGEAXXLDLRG 434
DB 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWDPSERPERFLETGAEGEARFDLRG 420

QY 435 XHFQLLPFGSGRXCWPCGVXKATLSGXTLLASLIQCFDLQVLGPOGQILKGDADKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKYSMEER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 11
US-09-857-581-20
; Sequence 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
; US-09-857-581-20
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QY 15 FXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLKDKLHYAXIDLKSKHGPFPSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLHYALIDLSKKGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 254
DB 181 ABEIRDIAREVLKIXGEYSLTDFIWPJLXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314
DB 241 VRRXNGEXVEGEASGVFLDILLFADETXEIKITKQIKGLVVDVFSAGTDSAVATE 300
QY 315 WALAELINNPVXXAREEYXVGVKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVKKR 374
DB 301 WALAELINNPVXXAREEYXVGVKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVKKR 360
QY 375 KCXECXINGVXPEGALXNFMVQGXDXKXVWDRPSEXPSEFRFLETXAEGEAXKLDLGR 434
DB 361 KCTECEINGVXPEGALXNFMVQGXDXKXVWDRPSEXPSEFRFLETXAEGEAGPLDLRG 420
QY 435 XHFQLLPFGSGRXXMCPGVXKATLGSXATLASLIQCFDLQVLGPGQOILKXDAKVSMEER 494
DB 421 QHFQLLPFGSGRXXMCPGVNLTSGMATLASLIQCFDLQVLGPGQOILKGDGDAKVSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 12
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: B81339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-22

Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;
QY 15 FXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLKDKLHYAXIDLKSKHGPFPSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLHYALIDLSKKGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120

QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 254
DB 181 ABEIRDIAREVLKIXGEYSLTDFIWPJLXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314
DB 241 VRRXNGEXVEGEASGVFLDILLFADETXEIKITKQIKGLVVDVFSAGTDSAVATE 300
QY 315 WALAELINNPVXXAREEYXVGVKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVKKR 374
DB 301 WALAELINNPVXXAREEYXVGVKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVKKR 360
QY 375 KCXECXINGVXPEGALXNFMVQGXDXKXVWDRPSEXPSEFRFLETXAEGEAXKLDLGR 434
DB 361 KCTECEINGVXPEGALXNFMVQGXDXKXVWDRPSEXPSEFRFLETXAEGEAGPLDLRG 420
QY 435 XHFQLLPFGSGRXXMCPGVXKATLGSXATLASLIQCFDLQVLGPGQOILKXDAKVSMEER 494
DB 421 XHFQLLPFGSGRXXMCPGVNLTSGMATLASLIQCFDLQVLGPGQOILKGDGDAKVSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 13
US-09-857-581-40
; Sequence 40, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: B81339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Trifolium repens
US-09-857-581-40

Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLKDKLHYAXIDLKSKHGPFPSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLHYALIDLSKKGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 254
DB 181 ABEIRDIAREVLKIXGEYSLTDFIWPJLXKLVGVYKXKIDDIILNKFPDVPVERVVKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314


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RESULT 16
US-09-857-581-57
; Sequence 57, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-57

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLKLLHYAXIDLKKGHGLPFSXX 74
Db 1 FLHLRPTPTAKSKALRHLPNPPSPKPRLPFFIGHLHLKDLKLLHYALIDLKKGHGLPFSLY 60
QY 75 FGSMPTVAVASTPELFLKFLQXEAATSFTRFQTSAXRLTYDXXVAXXPXGPMXKVRKL 134
Db 61 FGSMPTVAVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPMXKVRKL 120
QY 135 IMNDLLNATTNNKLRPLRTOQIRKLRMAQXABAKPLDTEELLKXNXTXSMXKLGE 194
Db 121 IMNDLLNATTNNKLRPLRTOQIRKLRVMAQGAQKPLDTEELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 254
Db 181 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXIKGLVVDXFSAGXDSTAXXTE 314
Db 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETXIKTKDHIKGLVVDXFSAGTDSVATE 300
QY 315 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
Db 301 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGVXPEGALXFNWQVGDXXKYWDRPSEXPXRPFLFETXAEGBAXXLDLGR 434
Db 361 KCTEECEINGVYIPEGALILFNWQVGRDPKYWDRPSEXPXRPFLFETGAEGBAXLDRG 420
QY 435 XHFQLLPFGSGRMCPCGVXATLTSXATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 494
Db 421 QHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 17
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLKLLHYAXIDLKKGHGLPFSXX 74
Db 1 FLHLRPTPTAKSKALRHLPNPPSPKPRLPFFIGHLHLKDLKLLHYALIDLKKGHGLPFSLY 60
QY 75 FGSMPTVAVASTPELFLKFLQXEAATSFTRFQTSAXRLTYDXXVAXXPXGPMXKVRKL 134
Db 61 FGSMPTVAVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPMXKVRKL 120
QY 135 IMNDLLNATTNNKLRPLRTOQIRKLRMAQXABAKPLDTEELLKXNXTXSMXKLGE 194
Db 121 IMNDLLNATTNNKLRPLRTOQIRKLRVMAQGAQKPLDTEELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 254
Db 181 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXIKGLVVDXFSAGXDSTAXXTE 314
Db 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETXIKTKDHIKGLVVDXFSAGTDSVATE 300
QY 315 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
Db 301 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGVXPEGALXFNWQVGDXXKYWDRPSEXPXRPFLFETXAEGBAXXLDLGR 434
Db 361 KCTEECEINGVYIPEGALILFNWQVGRDPKYWDRPSEXPXRPFLFETGAEGBAXLDRG 420
QY 435 XHFQLLPFGSGRMCPCGVXATLTSXATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 494
Db 421 QHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 18
US-09-857-581-38
; Sequence 38, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
```

```
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLKLLHYAXIDLKKGHGLPFSXX 74
Db 1 FLHLRPTPTAKSKALRHLPNPPSPKPRLPFFIGHLHLKDLKLLHYALIDLKKGHGLPFSLY 60
QY 75 FGSMPTVAVASTPELFLKFLQXEAATSFTRFQTSAXRLTYDXXVAXXPXGPMXKVRKL 134
Db 61 FGSMPTVAVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPMXKVRKL 120
QY 135 IMNDLLNATTNNKLRPLRTOQIRKLRMAQXABAKPLDTEELLKXNXTXSMXKLGE 194
Db 121 IMNDLLNATTNNKLRPLRTOQIRKLRVMAQGAQKPLDTEELLKXNXTXSMXKLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 254
Db 181 ABEIRDIAREVLKIXGEYSLDTFIPXPLKXKLVGKYEKRIIDILNKFPVVERVVKRXXI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXIKGLVVDXFSAGXDSTAXXTE 314
Db 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETXIKTKDHIKGLVVDXFSAGTDSVATE 300
QY 315 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
Db 301 WALAELINNPXYLXXAREEYXSVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGVXPEGALXFNWQVGDXXKYWDRPSEXPXRPFLFETXAEGBAXXLDLGR 434
Db 361 KCTEECEINGVYIPEGALILFNWQVGRDPKYWDRPSEXPXRPFLFETGAEGBAXLDRG 420
QY 435 XHFQLLPFGSGRMCPCGVXATLTSXATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 494
Db 421 QHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPGQQLKGDAXKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
```

```
RESULT 18
US-09-857-581-38
; Sequence 38, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
```


SOFTWARE: Microsoft Office 97
SEQ ID NO 38
LENGTH: 498
TYPE: PRT
ORGANISM: Trifolium repens
US-09-857-581-38

Query Match 95.9%; Score 2298; DB 1; Length 498;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 432; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

Qy	16	XHLRPTXAXSKALRHLNPNPSPXPRLPFFIGHLLKDLHLYAXIDLKKGCHPLFSXXF	75
Db	1	SHLRPTSAISKALRHLNPNPSPRPLPFFIGHLLKDLHLYAXIDLKKGCHPLFSLSF	60
Qy	76	GSMTVVASTPELFLQXKEATSFXTREFTQSAXRXLTYDXXVAXXPGPYWKFVRKLI	135
Db	61	GSMTVVASTPELFLQTHEATSFNTRFTQSARHLTYDNSVAVPGPYWKFVRKLI	120
Qy	136	MNDLLNATTNKLRLPTQOIRKXLRMAQXAEAKPLDXTBELLKXWNSIXSMXMLEA	195
Db	121	MNDLLNATTNKLRLPTQOIRKFLRYMAQSAEQKPLDXTBELLKWTNSTISMMMLGEA	180
Qy	196	BEIRDIAREVLKIXGEYSLTDFIPLKXKLVGKYEKIDIDILNKFPDPPVERVIKRRXIV	255
Db	181	BEIRDIAREVLKIFGEYSLTDFIPLKXKLVGKYEKIDIDILNKFPDPPVERVIKRRXIV	240
Qy	256	RRRXNGEXXGEXSGVXLDTLLEPAEDTBEIKITKXIKGLVVDXFSAGXDSTAXXTW	315
Db	241	RRRXNGEVVEGESVGLDITLLEPAEDTBEIKITKXIKGLVVDXFSAGTDSATAVTEW	300
Qy	316	ALAEILNPNVIXAREEYXSVGKDXLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR	375
Db	301	ALAEILNPNVIXAREEYXSVGKDXLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR	360
Qy	376	CXEECXINGVXPEGALXFNWVGDXDKYWDSPSEXPSEPERFLETXAEGEAXXLDLXG	435
Db	361	CXEECXINGVXPEGALXFNWVGDXDKYWDSPSEXPSEPERFLETXAEGEAXXLDLXG	420
Qy	436	HFQLLPFGSGRMCPGVXLTSGXATLLASLIQCFLDQVLGPGQIILKXDAKVSMEERA	495
Db	421	HFQLLPFGSGRMCPGVXLTSGXATLLASLIQCFLDQVLGPGQIILKXDAKVSMEERA	480
Qy	496	GLTVPRAHSLVCVPLARI	513
Db	481	GLTVPRAHSLVCVPLARI	498

RESULT 19

US-09-857-581-61
Sequence 61, Application US/09857581
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BBI339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 61
LENGTH: 498
TYPE: PRT
ORGANISM: Beta vulgaris
US-09-857-581-61

Query Match 95.7%; Score 2293; DB 1; Length 498;
Best Local Similarity 86.5%; Pred. No. 0;

Matches 431; Conservative 66; Mismatches 1; Indels 0; Gaps 0;

Qy	16	XHLRPTXAXSKALRHLNPNPSPXPRLPFFIGHLLKDLHLYAXIDLKKGCHPLFSXXF	75
Db	1	LHLRPTTAKSKALRHLNPNPSPKPRLPFFIGHLLKDLHLYALIDLKKGCHPLFSHYF	60
Qy	76	GSMTVVASTPELFLQXKEATSFXTREFTQSAXRXLTYDXXVAXXPGPYWKFVRKLI	135
Db	61	GSMTVVASTPELFLQTNTEATSFNTRFTQSARHLTYDSSVAVPGPYWKFVRKLI	120
Qy	136	MNDLLNATTNKLRLPTQOIRKXLRMAQXAEAKPLDXTBELLKXWNSIXSMXMLEA	195
Db	121	MNDLLNATTNKLRLPTQOIRKFLRYMAQSAEQKPLDXTBELLKWNSTISMMMLGEA	180
Qy	196	BEIRDIAREVLKIXGEYSLTDFIPLKXKLVGKYEKIDIDILNKFPDPPVERVIKRRXIV	255
Db	181	BEIRDIAREVLKIFGEYSLTDFIPLKXKLVGKYEKIDIDILNKFPDPPVERVIKRRXIV	240
Qy	256	RRRXNGEXXGEXSGVXLDTLLEPAEDTBEIKITKXIKGLVVDXFSAGXDSTAXXTW	315
Db	241	RRRXNGEVVEGESVGLDITLLEPAEDTBEIKITKXIKGLVVDXFSAGTDSATAVTEW	300
Qy	316	ALAEILNPNVIXAREEYXSVGKDXLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR	375
Db	301	ALAEILNPNVIXAREEYXSVGKDXLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR	360
Qy	376	CXEECXINGVXPEGALXFNWVGDXDKYWDSPSEXPSEPERFLETXAEGEAXXLDLXG	435
Db	361	CXEECXINGVXPEGALXFNWVGDXDKYWDSPSEXPSEPERFLETXAEGEAXXLDLXG	420
Qy	436	HFQLLPFGSGRMCPGVXLTSGXATLLASLIQCFLDQVLGPGQIILKXDAKVSMEERA	495
Db	421	HFQLLPFGSGRMCPGVXLTSGXATLLASLIQCFLDQVLGPGQIILKXDAKVSMEERA	480
Qy	496	GLTVPRAHSLVCVPLARI	513
Db	481	GLTVPRAHSLVCVPLARI	498

Search completed: February 26, 2004, 16:59:38
Job time: 3 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 07:06:46 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: af135484pep
Perfect score: 2679
Sequence: 1 MLELALGLLVIALFLHLP.....AHSILVCVPLARIGVASKLS 521

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues
Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2667	99.6	521	1	US-09-857-581-26
2	2667	99.6	522	1	US-09-857-581-24
3	2665	99.5	521	1	US-09-857-581-28
4	2665	99.5	521	1	US-09-857-581-30
5	2665	99.5	521	1	US-09-857-581-34
6	2652	99.0	521	1	US-09-857-581-32
7	2614	97.6	521	1	US-09-857-581-2
8	2596	96.9	521	1	US-09-857-581-36
9	2563	95.7	499	1	US-09-857-581-59
10	2554	95.3	499	1	US-09-857-581-22
11	2553	95.3	499	1	US-09-857-581-48
12	2548	95.1	499	1	US-09-857-581-18
13	2544	95.0	499	1	US-09-857-581-55
14	2539	94.8	499	1	US-09-857-581-57
15	2528	94.4	499	1	US-09-857-581-40
16	2525	94.3	499	1	US-09-857-581-61
17	2519	94.0	499	1	US-09-857-581-20
18	2498	93.2	499	1	US-09-857-581-16
19	2473	92.3	498	1	US-09-857-581-38

ALIGNMENTS

RESULT 1
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
; US-09-857-581-26

Query Match 99.6%; Score 2667; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MLELALGLLVIALFLHLPPTAKSKALRHLPNPSPKPRLPFFIGHLLKDKLLHYAL	60
DB	1	MLELALGLLVIALFLHLPPTAKSKALRHLPNPSPKPRLPFFIGHLLKDKLLHYAL	60
QY	61	IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHEATSFNTRFQTSAIRRLTYDSSVA	120
DB	61	IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHEATSFNTRFQTSAIRRLTYDSSVA	120
QY	121	MVPFGPYKFKRLIMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDTEELL	180
DB	121	MVPFGPYKFKRLIMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDTEELL	180
QY	181	KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLDFIWPPLKHLKVGKYEKIDILNKF	240
DB	181	KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLDFIWPPLKHLKVGKYEKIDILNKF	240
QY	241	DPVVERVIKRRREIVRRRNKNGEVSGVPLDTLLFEAEDTWEIKTKDHKIGLVVD	300
DB	241	DPVVERVIKRRREIVRRRNKNGEVSGVPLDTLLFEAEDTWEIKTKDHKIGLVVD	300
QY	301	FSAGTDSATAVATEWALAEILNNPKVLEKAREVSVVGKDLVDEVDTONLPYIRAIYK	360
DB	301	FSAGTDSATAVATEWALAEILNNPKVLEKAREVSVVGKDLVDEVDTONLPYIRAIYK	360
QY	361	ETFRMHPPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWRPSPFRERFLE	420
DB	361	ETFRMHPPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWRPSPFRERFLE	420
QY	421	TGABEGAGPLDLRGQHFQLLPTGSGRMCPCGVNLTSGMATLLASLIQCDFIQLVGPQQ	480
DB	421	TGABEGAGPLDLRGQHFQLLPTGSGRMCPCGVNLTSGMATLLASLIQCDFIQLVGPQQ	480
QY	481	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLS	521
DB	481	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLS	521

RESULT 2
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match      99.6%; Score 2667; DB 1; Length 522;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60
Db 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60

QY 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Db 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

QY 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLTDFIWLPLKLVKGYEKRIDDIILNKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLTDFIWLPLKLVKGYEKRIDDIILNKF 240

QY 241 DPVVERVIKKREIIVRRKNGEVEGVSGLVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300
Db 241 DPVVERVIKKREIIVRRKNGEVEGVSGLVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300

QY 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEYVSVGKORLVDEVDTQNLPIYRAIVK 360
Db 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEYVSVGKORLVDEVDTQNLPIYRAIVK 360

QY 361 ETRFRMHPPLPVVKRKCTECEEINGVYIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFRMHPPLPVVKRKCTECEEINGVYIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPOGQ 480
Db 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFLQVLGPOGQ 480

QY 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 4
US-09-857-581-30
; Sequence 30, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-30

Query Match      99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60
Db 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60

QY 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Db 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

Query Match      99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60
Db 1 MLELALGLLVLFHLPPTPTAKSKALRHLNPNPSPKPLPFIHHLHLKOKLLHYAL 60

QY 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGFLFSLYFGSMPTVASTPELFLQTHQTSFNTFRQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Db 121 MYPFGPYKRFVRLIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
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Db 121 MPPFGPVKKVVKLIMNDLLNATVVKLRPLRTQIQIRKFLRVWAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Db 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 5
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLFALFLHLPRTPTAKSKALRHLPNPPSPKPLPFIHLLHLLKDLHYAL 60
Db 1 MLELALGLLVLFALFLHLPRTPTAKSKALRHLPNPPSPKPLPFIHLLHLLKDLHYAL 60
Qy 61 IDLSKXGHPFLSLYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKXGHPFLSLYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPFGPVKKVVKLIMNDLLNATVVKLRPLRTQIQIRKFLRVWAQGAQKPLDLTEELL 180
Db 121 MPPFGPVKKVVKLIMNDLLNATVVKLRPLRTQIQIRKFLRVWAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Db 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
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Db 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 6
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR FILING DATE: 60/117,769
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 99.0%; Score 2652; DB 1; Length 521;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 517; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLFALFLHLPRTPTAKSKALRHLPNPPSPKPLPFIHLLHLLKDLHYAL 60
Db 1 MLELALGLLVLFALFLHLPRTPTAKSKALRHLPNPPSPKPLPFIHLLHLLKDLHYAL 60
Qy 61 IDLSKXGHPFLSLYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKXGHPFLSLYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPFGPVKKVVKLIMNDLLNATVVKLRPLRTQIQIRKFLRVWAQGAQKPLDLTEELL 180
Db 121 MPPFGPVKKVVKLIMNDLLNATVVKLRPLRTQIQIRKFLRVWAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGAEABEIRDIAREVLKIFGYSLSLTDPIWPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Db 241 DPVVERVVKRREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKHIGKLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEYVSVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
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QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521

RESULT 7
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2

Query Match 97.6%; Score 2614; DB 1; Length 521;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 507; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPRTPTAKSKALRHLNPPSPKPLPFIHLLKDLHYAL 60
Db 1 MLELALGLFVLALFHLRPTPSAKSKALRHLNPPSPKPLPFIHLLKDLHYAL 60

QY 61 IDLSKHGFLPSLFGSMPTVASTPELFLQTHAETSNTFRPQTSARRLTYSVA 120
Db 61 IDLSKHGFLPSLFGSMPTVASTPELFLQTHAETSNTFRPQTSARRLTYSVA 120

QY 121 MYPFGPYKFKVKLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAQAQPLDTELL 180
Db 121 MYPFGPYKFKVKLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAQAQPLDTELL 180

QY 181 KWTNSTISMMMLGEAEIRDIAREVLFGEYSLTDFIWLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLFGEYSLTDFIWLKHLKVGKYEKRIDDILNKF 240

QY 241 DPWVERVIKKREIVRRRKNQGEVGEVSGVFLDTLLEFADETMETIKTDHIKGLVVD 300
Db 241 DPWVERVIKKREIVRRRKNQGEVGEVSGVFLDTLLEFADETMETIKTDHIKGLVVD 300

QY 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIRAIVK 360
Db 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIRAIVK 360

QY 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521
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RESULT 8
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36

Query Match 96.9%; Score 2596; DB 1; Length 521;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 502; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPRTPTAKSKALRHLNPPSPKPLPFIHLLKDLHYAL 60
Db 1 MLELALGLFVLALFHLRPTPSAKSKALRHLNPPSPKPLPFIHLLKDLHYAL 60

QY 61 IDLSKHGFLPSLFGSMPTVASTPELFLQTHAETSNTFRPQTSARRLTYSVA 120
Db 61 IDLSKHGFLPSLFGSMPTVASTPELFLQTHAETSNTFRPQTSARRLTYSVA 120

QY 121 MYPFGPYKFKVKLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAQAQPLDTELL 180
Db 121 MYPFGPYKFKVKLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAQAQPLDTELL 180

QY 181 KWTNSTISMMMLGEAEIRDIAREVLFGEYSLTDFIWLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLFGEYSLTDFIWLKHLKVGKYEKRIDDILNKF 240

QY 241 DPWVERVIKKREIVRRRKNQGEVGEVSGVFLDTLLEFADETMETIKTDHIKGLVVD 300
Db 241 DPWVERVIKKREIVRRRKNQGEVGEVSGVFLDTLLEFADETMETIKTDHIKGLVVD 300

QY 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIRAIVK 360
Db 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIRAIVK 360

QY 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
Db 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPAHSLVCVPLARIGVASKILLS 521
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RESULT 9
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
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; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match      95.7%; Score 2563; DB 1; Length 499;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 495; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 15 FLHLRPTPTAKSKALRHLNPPSPKPRLPFTIGHLLKDKLLHYALIDLSKKGHPPLFSLY 74
Db 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFTIGHLLKDKLLHYALIDLSKKGHPPLFSLY 60

Qy 75 FGSMTVVASTPELFLQTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 134
Db 61 FGSMTVVASTPELFLQTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 120

Qy 135 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTTELLKWTNSTISMMLGE 194
Db 121 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTTELLKWTNSTISMMLGE 180

Qy 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 254
Db 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 240

Qy 255 VRRKNGEVEGEVSGVFLDTLLFAEDTWEIKITKDHIKGLVDPFSSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLFAEDTWEIKITKDHIKGLVDPFSSAGTDSAVATE 300

Qy 315 WALAEILNNPKVLEKAREEVSVVGKDRLVDEVDTONLPYIRALVKETFRMHHPPLPVVXR 374
Db 301 WALAEILNNPKVLEKAREEVSVVGKDRLVDEVDTONLPYIRALVKETFRMHHPPLPVVXR 360

Qy 375 KCTEECEINGVIVEGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRG 434
Db 361 KCTEECEINGVIVEGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRG 420

Qy 435 QHFOLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 494
Db 421 QHFOLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 480

Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
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; SEQ ID NO 22
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-22

Query Match      95.3%; Score 2554; DB 1; Length 499;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 494; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 15 FLHLRPTPTAKSKALRHLNPPSPKPRLPFTIGHLLKDKLLHYALIDLSKKGHPPLFSLY 74
Db 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFTIGHLLKDKLLHYALIDLSKKGHPPLFSLY 60

Qy 75 FGSMTVVASTPELFLQTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 134
Db 61 FGSMTVVASTPELFLQTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 120

Qy 135 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTTELLKWTNSTISMMLGE 194
Db 121 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTTELLKWTNSTISMMLGE 180

Qy 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 254
Db 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 240

Qy 255 VRRKNGEVEGEVSGVFLDTLLFAEDTWEIKITKDHIKGLVDPFSSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLFAEDTWEIKITKDHIKGLVDPFSSAGTDSAVATE 300

Qy 315 WALAEILNNPKVLEKAREEVSVVGKDRLVDEVDTONLPYIRALVKETFRMHHPPLPVVXR 374
Db 301 WALAEILNNPKVLEKAREEVSVVGKDRLVDEVDTONLPYIRALVKETFRMHHPPLPVVXR 360

Qy 375 KCTEECEINGVIVEGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRG 434
Db 361 KCTEECEINGVIVEGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRG 420

Qy 435 QHFOLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 494
Db 421 QHFOLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 480

Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 11
US-09-857-581-48
; Sequence 48, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 48
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-48

Query Match      95.3%; Score 2553; DB 1; Length 499;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 15 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 60
QY 75 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 134
DB 61 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 120
QY 135 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 194
DB 121 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 240
QY 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314
DB 241 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVVKR 360
QY 375 KCTECEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRG 434
DB 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKVSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKVSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 12
US-09-857-581-18
; Sequence 18, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 60/117,769
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 60/144,783
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Vicia villosa
US-09-857-581-18

Query Match 95.1%; Score 2548; DB 1; Length 499;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 493; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 15 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 60
QY 75 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 134
DB 61 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 120
```

```
QY 135 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 194
DB 121 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 240
QY 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314
DB 241 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVVKR 360
QY 375 KCTECEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRG 434
DB 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKVSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOGQILKGGDAKVSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 13
US-09-857-581-55
; Sequence 55, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lupinus albus
US-09-857-581-55

Query Match 95.0%; Score 2544; DB 1; Length 499;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 493; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 15 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTPTAKSKALRHLNPPSPKPLPFIHGLHLLKDKLLHVALIDLSKKHGPLFSLY 60
QY 75 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 134
DB 61 FGSMTVWASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKWKFVRKL 120
QY 135 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 194
DB 121 IMNDLLNATTNKLRLPRTQOIRKFLRVMAQGAQAQKPLDLTBEILLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSYSLDFIWLPLKHLKVGKYEKRIDDILNKFDVVERVVKRREI 240
QY 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314
```



```
RESULT 16
US-09-857-581-61
; Sequence 61, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 61
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-61

Query Match 94.3%; Score 2525; DB 1; Length 498;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 489; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 16 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLPSLYF 75
Db 1 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLPSHYF 60

QY 76 GSMPTVASTPELFLQTHAETSFNTRFQTSAIRLTYDSSVAMVPFGPYKFKVKLI 135
Db 61 GSMPTVASTPELFLQTHAETSFNTRFQTSAIRLTYDSSVAMVPFGPYKFKVKLI 120

QY 136 MNDLLNATTVNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTELLKWTNSTISMMMLGEA 195
Db 121 MNDLLNATTVNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTELLKWTNSTISMMMLGEA 180

QY 196 BEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREIV 255
Db 181 BEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREIV 240

QY 256 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFFSAGTDSAVATEW 315
Db 241 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFFSAGTDSAVATEW 300

QY 316 ALAEILNNPKVLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRK 375
Db 301 ALAEILNNPKVLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRK 360

QY 376 CTECEINGYVPEGALIFNVQGRDPKYWDRESEFRPERFLETGAEGAGPLDLRGQ 435
Db 361 CTECEINGYVPEGALIFNVQGRDPKYWDRESEFRPERFLETGAEGAGPLDLRGQ 420

QY 436 HFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEERA 495
Db 421 HFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEERA 480

QY 496 GLTVPRASHLVCVPLARI 513
Db 481 GLTVPRASHLVCVPLARI 498

RESULT 17
US-09-857-581-20
; Sequence 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-20

Query Match 94.0%; Score 2519; DB 1; Length 499;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 486; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 15 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLPSLY 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLPSLY 60

QY 75 FGSMPTVASTPELFLQTHAETSFNTRFQTSAIRLTYDSSVAMVPFGPYKFKVKRL 134
Db 61 FGSMPTVASTPELFLQTHAETSFNTRFQTSAIRLTYDSSVAMVPFGPYKFKVKRL 120

QY 135 IMNDLLNATTVNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTELLKWTNSTISMMMLGE 194
Db 121 IMNDLLNATTVNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTELLKWTNSTISMMMLGE 180

QY 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 240

QY 255 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFFSAGTDSAVATE 314
Db 241 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFFSAGTDSAVATE 300

QY 315 WALAEILNNPKVLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRK 374
Db 301 WALAEILNNPKVLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRK 360

QY 375 KCTECEINGYVPEGALIFNVQGRDPKYWDRESEFRPERFLETGAEGAGPLDLRG 434
Db 361 KCTECEINGYVPEGALIFNVQGRDPKYWDRESEFRPERFLETGAEGAGPLDLRG 420

QY 435 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 18
US-09-857-581-16
; Sequence 16, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-16
```

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 16

; LENGTH: 499

; TYPE: PRT

; ORGANISM: Medicago sativa

US-09-857-581-16

Query Match 93.2%; Score 2498; DB 1; Length 499;

Best Local Similarity 96.4%; Pred. No. 0;

Matches 481; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```
QY 15 FLHLRPTAKSKALRHLNPPSPKPELPFIHLLHLLKOKLLHYALIDLSKKGHPFSLY 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 FLHLRPTSAKSKALRHLNPPSPKPELPFIHLLHLLKOKLLHYALIDLSKKGHPFSL 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 75 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPGPYKVRKL 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPGPYKVRKL 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 135 IMNDLLNATTVNKLRLPTQOIRKFLRVMAQGAEOAKPLDLTTELLKWTNSTISMMMLGE 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 IMNDLLNATTVNKLRLPTQOIRKFLRVMAQGAEOAKPLDLTTELLKWTNSTISMMMLGE 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 195 ABEIRDIAREVLKIFGEYSLTDFIWP.LKHLKVGYEKRIDDILNKFPDPVVERVIKKRREI 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWP.LKHLKVGYEKRIDDILNKFPDPVVERVIKKRGI 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 VRRKNGEVVEGEVSGVFLDTLLLEFADETMELKITKDHKGLVDPFFSAGTSTAVATE 314
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 VRRKNGEVVEGEVSGVFLDTLLLEFADETMELKITKDHKGLVDPFFSAGTSTAVATE 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 315 WALAELINNPKVLEKAREEYVSVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKR 374
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 WALAELINNPRVLQKAREEYVSVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKR 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 375 KCTECCINGVVIPEGALILFNWQVGRDPKYWDRPSEPRPERFLETGAEAGEAGPLDLRG 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 KCTECCINGVVIPEGALVLFNMQVGRDPKYWDRPSEPRPERFLETGAEAGEAGPLDLRG 420
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 435 QHFOLLPFGSRRCMCPGVNLSATSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSMEER 494
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 QHFOLLPFGSRRCMCPGVNLSATSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSMEER 480
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 495 AGLTVPRAHSLVCVPLARI 513
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 AGLTVPRAHSLVCVPLARI 499
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 19

US-09-857-581-38

; Sequence 38, Application US/09857581

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

; FILE REFERENCE: B81339 PCT

; CURRENT APPLICATION NUMBER: US/09/857,581

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769

; PRIOR FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: 60/144,783

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 60/156,094

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 38

; LENGTH: 498

; TYPE: PRT

; ORGANISM: Trifolium repens

US-09-857-581-38

Query Match

Best Local Similarity 92.3%; Score 2473; DB 1; Length 498;

Matches 496; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

```
Matches 477; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 17 HLRLPTAKSKALRHLNPPSPKPELPFIHLLHLLKOKLLHYALIDLSKKGHPFSLYFG 76
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 HLRLPTSAKSKALRHLNPPSPKPELPFIHLLHLLKOKLLHYALIDLSKKGHPFSLYFG 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 77 SMTPTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPGPYKVRKLIM 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 SMTPTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPGPYKVRKLIM 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 137 NDLLNATTVNKLRLPTQOIRKFLRVMAQGAEOAKPLDLTTELLKWTNSTISMMMLGEAE 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 NDLLNATTVNKLRLPTQOIRKFLRVMAQGAEOAKPLDLTTELLKWTNSTISMMMLGEAE 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 EIRDIAREVLKIFGEYSLTDFIWP.LKHLKVGYEKRIDDILNKFPDPVVERVIKKRREIVR 256
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 EIRDIAREVLKIFGEYSLTDFIWP.LKHLKVGYEKRIDDILNKFPDPVVERVIKKRREIVR 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 257 RKNNGEVVEGEVSGVFLDTLLLEFADETMELKITKDHKGLVDPFFSAGTSTAVATEWA 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 RKNNGEVVEGEVSGVFLDTLLLEFADETMELKITKDHKGLVDPFFSAGTSTAVATEWA 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 317 LAELINNPKVLEKAREEYVSVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRKC 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 LAELINNPRVLQKAREEYVSVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRKC 361
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 377 TEECEINGVVIPEGALILFNWQVGRDPKYWDRPSEPRPERFLETGAEAGEAGPLDLRGQH 436
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 TEECEINGVVIPEGALVLFNMQVGRDPKYWDRPSEPRPERFLETGAEAGEAGPLDLRGQH 421
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 437 FOLLPFGSRRCMCPGVNLSATSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSMEERAG 496
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 FOLLPFGSRRCMCPGVNLSATSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSMEERAG 481
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 497 LTVPRAHSLVCVPLARI 513
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 LTVPRAHSLVCVPLARI 498
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: March 1, 2004, 07:06:48

Job time : 2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 07:04:37 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: af022462pep
Perfect score: 2583
Sequence: 1 MLELALGLLVLFHLP.....AHSILVCVPLARIGVASKLLS 521

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2651	98.8	521	1	US-09-857-581-26
2	2651	98.8	522	1	US-09-857-581-24
3	2649	98.7	521	1	US-09-857-581-28
4	2649	98.7	521	1	US-09-857-581-30
5	2649	98.7	521	1	US-09-857-581-34
6	2636	98.2	521	1	US-09-857-581-32
7	2598	96.8	521	1	US-09-857-581-2
8	2580	95.2	521	1	US-09-857-581-36
9	2547	94.9	499	1	US-09-857-581-59
10	2538	94.6	499	1	US-09-857-581-22
11	2537	94.6	499	1	US-09-857-581-48
12	2532	94.4	499	1	US-09-857-581-18
13	2528	94.2	499	1	US-09-857-581-55
14	2523	94.0	499	1	US-09-857-581-57
15	2512	93.6	499	1	US-09-857-581-40
16	2509	93.5	498	1	US-09-857-581-61
17	2503	93.3	499	1	US-09-857-581-20
18	2482	92.5	499	1	US-09-857-581-16
19	2457	91.6	498	1	US-09-857-581-38

ALIGNMENTS

RESULT 1
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-26

Query Match 98.8%; Score 2651; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPPTAKSKALRHLNPPSPKRLPFTFCHLHLKDLHYAL 60
DB 1 MLELALGLLVLFHLPPTAKSKALRHLNPPSPKRLPFTFCHLHLKDLHYAL 60

QY 61 IDLSKKGHPFLSYFGSMPTVVASTPELPKLPLOTHEATSFNTRPOTSAIRRLTYDSSVA 120
DB 61 IDLSKKGHPFLSYFGSMPTVVASTPELPKLPLOTHEATSFNTRPOTSAIRRLTYDSSVA 120

QY 121 MYPFGPYMKFVKLIWMDLNPATTVNKLRLPTQOTRFLRVMAQCAQAQKPLDLTEELL 180
DB 121 MYPFGPYMKFVKLIWMDLNPATTVNKLRLPTQOTRFLRVMAQCAQAQKPLDLTEELL 180

QY 181 KWTNSTISMMMLGEAEIRDIAREVLKIPGEVSLTDFIWPMLKLVKGYKEKIDILNKF 240
DB 181 KWTNSTISMMMLGEAEIRDIAREVLKIPGEVSLTDFIWPMLKLVKGYKEKIDILNKF 240

QY 241 DPVVERVIKRRREIVRRKNGEVGEVSGVFLDTLLEPADETEIKITKHIGLVVD 300
DB 241 DPVVERVIKRRREIVRRKNGEVGEVSGVFLDTLLEPADETEIKITKHIGLVVD 300

QY 301 FFSAGTSDTAVATEWALAEILNPNKVKLEKAREEVSVVGKRLVDEVDTONLPYIRAIYK 360
DB 301 FFSAGTSDTAVATEWALAEILNPNKVKLEKAREEVSVVGKRLVDEVDTONLPYIRAIYK 360

QY 361 EFRMHPPVPVVKRCKTECEINGVYIPGAILFNWGVGDPKYWDPSFRFRERFLE 420
DB 361 EFRMHPPVPVVKRCKTECEINGVYIPGAILFNWGVGDPKYWDPSFRFRERFLE 420

QY 421 TGAEGAGPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOGQ 480
DB 421 TGAEGAGPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOGQ 480

QY 481 ILKGGDAKVMBEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
DB 481 ILKGGDAKVMBEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24

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; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match      98.8%; Score 2651; DB 1; Length 522;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60
Db 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60

Qy 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180

Qy 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSITDFTWPLKHLKVGKYEKRIIDILNKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSITDFTWPLKHLKVGKYEKRIIDILNKF 240

Qy 241 DPVVERVIKGRREIVRRKNGEVEGVSFVLDLTLLFAEDTMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKGRREIVRRKNGEVEGVSFVLDLTLLFAEDTMEIKITKDHIEGLVVD 300

Qy 301 PFSAGTDSATATEWALAEALINNPVLEKAREEVSUVGKDRLVDEVDTONLPYIRAIK 360
Db 301 PFSAGTDSATATEWALAEALINNPVLEKAREEVSUVGKDRLVDEVDTONLPYIRAIK 360

Qy 361 ETRFMHPPLPVVKRKTCECEINGYVPEGALILFNVMQVGRDPKYMDRPSSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRKTCECEINGYVPEGALILFNVMQVGRDPKYMDRPSSEFRPERFLE 420

Qy 421 TGAEGEAPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQ 480
Db 421 TGAEGEAPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQ 480

Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 4
US-09-857-581-30
; Sequence 30, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-30

Query Match      98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60
Db 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60

Qy 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180

Query Match      98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60
Db 1 MLELALGLLVLFALFHLRPTPTAKSKALRHLNPPSPKRLPFIHGLHLKDKLHYAL 60

Qy 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPFLSIFYGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTVNKLRLPRTQOTRKFLEVMQAQGAOKPLDLTEELL 180

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Db 121 MPPGPGYKFKVRKLIIMNDLLNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Qy 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDVLGPQGG 480
Db 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 5
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKRLPFIHLLHLLKDLHYAL 60
Db 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKRLPFIHLLHLLKDLHYAL 60
Qy 61 IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHREATSFNTREFTQSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHREATSFNTREFTQSAIRRLTYDSSVA 120
Qy 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Db 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
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Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Qy 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDVLGPQGG 480
Db 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 6
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 98.2%; Score 2636; DB 1; Length 521;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 514; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKRLPFIHLLHLLKDLHYAL 60
Db 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKRLPFIHLLHLLKDLHYAL 60
Qy 61 IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHREATSFNTREFTQSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPFLSLYFGSMPTVASTPELFLQTHREATSFNTREFTQSAIRRLTYDSSVA 120
Qy 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Db 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSAVATWALAEALINNPKVLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNWQVGRPKYWDPSSEFRPFLE 420
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QY 421 TGAEGAGLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGEARPLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 7
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2

Query Match 96.8%; Score 2598; DB 1; Length 521;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 504; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 MLELALGLLVLTALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHLLKDKLLHYAL 60
Db 1 MLELALGLFVLALFLHLRPTSPAKSKALRHLPNPPSPKPLPFIHLLKDKLLHYAL 60
QY 61 IDLSKXHGPLFSLYFGSMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGPLFSLYFGSMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
QY 121 MYPFGPYNKFVVKLIINDDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
Db 121 MYPFGPYNKFVVKLIINDDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
QY 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIDDILNKF 240
QY 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLFEAEDTMEIKITKHIEGLVVD 300
Db 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLFEAEDTMEIKITKHIEGLVVD 300
QY 301 FFSAGTDSATAWALAEILNNPKVLBKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAWALAEILNNPKVLBKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
QY 361 ETRFMHPPLPVVKRKCTECEINGVYIPGALILFNVQVGRDPKYWDPSRPERFLE 420
Db 361 ETRFMHPPLPVVKRKCTECEINGVYIPGALILFNVQVGRDPKYWDPSRPERFLE 420
QY 421 TGAEGAGLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGAGLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 8
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36
Query Match 96.2%; Score 2580; DB 1; Length 521;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 499; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MLELALGLLVLTALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHLLKDKLLHYAL 60
Db 1 MLELALGLFVLALFLHLRPTSPAKSKALRHLPNPPSPKPLPFIHLLKDKLLHYAL 60
QY 61 IDLSKXHGPLFSLYFGSMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGPLFSLYFGSMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
QY 121 MYPFGPYNKFVVKLIINDDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
Db 121 MYPFGPYNKFVVKLIINDDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
QY 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIDDILNKF 240
QY 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLFEAEDTMEIKITKHIEGLVVD 300
Db 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLFEAEDTMEIKITKHIEGLVVD 300
QY 301 FFSAGTDSATAWALAEILNNPKVLBKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAWALAEILNNPKVLBKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
QY 361 ETRFMHPPLPVVKRKCTECEINGVYIPGALILFNVQVGRDPKYWDPSRPERFLE 420
Db 361 ETRFMHPPLPVVKRKCTECEINGVYIPGALILFNVQVGRDPKYWDPSRPERFLE 420
QY 421 TGAEGAGLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
Db 421 TGAEGAGLDLRGQHQLLPPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQGG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 9
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581

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; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match
Best Local Similarity 94.9%; Score 2547; DB 1; Length 499;
Matches 492; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 15 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLLHYALIDLSKKGGLPFSLY 74
DB 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLLHYALIDLSKKGGLPFSLY 60
QY 75 FGSMTVAVASTPELFKFLQTHEATSFNTRFQTSAIRRLTYDSSVAVPFGPYWKFVRKL 134
DB 61 FGSMTVAVASTPELFKFLQTHEATSFNTRFQTSAIRRLTYDSSVAVPFGPYWKFVRKL 120
QY 135 IMNDLPNATTNKLRLPTQOTRKFLRVMAQGAQAQKPLDLTEELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNKLRLPTQOTRKFLRVMAQGAQAQKPLDLTEELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 240
QY 255 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDFFSAGTSTAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDFFSAGTSTAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVMGKDLVDEVDTONLPYIRAIYKETFMRHPPPLPVVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVMGKDLVDEVDTONLPYIRAIYKETFMRHPPPLPVVVKR 360
QY 375 KCTECEINGYVIPGALILFNWQVGRDPKYWDPRSEFRPERFLETGAEAGEAPLDLRG 434
DB 361 KCTECEINGYVIPGALILFNWQVGRDPKYWDPRSEFRPERFLETGAEAGEAPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPGQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPGQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 48
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-48

Query Match
Best Local Similarity 94.6%; Score 2537; DB 1; Length 499;
Matches 492; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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QY 15 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 60
QY 75 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDILLEFAEDTMEIKITKDHIEGLVVDFFSAGTDSAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDILLEFAEDTMEIKITKDHIEGLVVDFFSAGTDSAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVDKRLVDEVDTONLPYIRAIKVFTRFMHPPLPVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVDKRLVDEVDTONLPYIRAIKVFTRFMHPPLPVVKR 360
QY 375 KCTECEINGYVIPGALILFNWQVGRDPKYWDPSFRPERFLETGAEGEARLLDLRG 434
DB 361 KCTECEINGYVIPGALILFNWQVGRDPKYWDPSFRPERFLETGAEGEARLLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
RESULT 12
US-09-857-581-18
; Sequence 18, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Vicia villosa
US-09-857-581-18
Query Match 94.4%; Score 2532; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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QY 15 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 60
QY 75 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
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QY 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDILLEFAEDTMEIKITKDHIEGLVVDFFSAGTDSAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDILLEFAEDTMEIKITKDHIEGLVVDFFSAGTDSAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVDKRLVDEVDTONLPYIRAIKVFTRFMHPPLPVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVDKRLVDEVDTONLPYIRAIKVFTRFMHPPLPVVKR 360
QY 375 KCTECEINGYVIPGALILFNWQVGRDPKYWDPSFRPERFLETGAEGEARLLDLRG 434
DB 361 KCTECEINGYVIPGALILFNWQVGRDPKYWDPSFRPERFLETGAEGEARLLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
RESULT 13
US-09-857-581-55
; Sequence 55, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lupinus albus
US-09-857-581-55
Query Match 94.2%; Score 2528; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 15 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKRLPFIQHLHLKDLKLLHYALIDLSKKGGLPFLSLY 60
QY 75 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPFLPKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDVPVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDILLEFAEDTMEIKITKDHIEGLVVDFFSAGTDSAVATE 314
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Db 241 VRRKNGVEGEVSGVLLDTLLEFADETEWEIKITKDHKGLVDFFSAGTSTAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 14
US-09-857-581-57
; Sequence 57, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-57

Query Match 94.0%; Score 2523; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 15 FLHLRPTTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYALIDLSKKHGPLPSLY 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYALIDLSKKHGPLPSLY 60
Qy 75 FGSMTVVASTPELPFKLFLOTHATSNTFRQTSAIRRLTYDSSVAMVPPGPKFVRKL 134
Db 61 FGSMTVVASTPELPFKLFLOTHATSNTFRQTSAIRRLTYDSSVAMVPPGPKFVRKL 120
Qy 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTLLELLKWTNSTISMMMLGE 194
Db 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTLLELLKWTNSTISMMMLGE 180
Qy 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVVKRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVVKRREI 240
Qy 255 VRRKNGVEGEVSGVFLDTLLEFADETEWEIKITKDHIEGLVDFFSAGTSTAVATE 314
Db 241 VRRKNGVEGEVSGVFLDTLLEFADETEWEIKITKDHIEGLVDFFSAGTSTAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
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Db 361 KCTECEINGVVIPEGALILFNVMQVGRDSKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 15
US-09-857-581-40
; Sequence 40, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Trifolium repens
US-09-857-581-40

Query Match 93.6%; Score 2512; DB 1; Length 499;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 484; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 15 FLHLRPTTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYALIDLSKKHGPLPSLY 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYALIDLSKKHGPLPSLY 60
Qy 75 FGSMTVVASTPELPFKLFLOTHATSNTFRQTSAIRRLTYDSSVAMVPPGPKFVRKL 134
Db 61 FGSMTVVASTPELPFKLFLOTHATSNTFRQTSAIRRLTYDSSVAMVPPGPKFVRKL 120
Qy 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTLLELLKWTNSTISMMMLGE 194
Db 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQKPLDTLLELLKWTNSTISMMMLGE 180
Qy 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVVKRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVVKRREI 240
Qy 255 VRRKNGVEGEVSGVFLDTLLEFADETEWEIKITKDHIEGLVDFFSAGTSTAVATE 314
Db 241 VRRKNGVEGEVSGVFLDTLLEFADETEWEIKITKDHIEGLVDFFSAGTSTAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFETFRMHPLPVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSRRMCPGVNLTATSGMATLLASLIQCFDQVLVGPQOILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
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RESULT 16
US-09-857-581-61
; SEQUENCE 61, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 61
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-61

Query Match      93.5%; Score 2509; DB 1; Length 498;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 486; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 16 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKGHGLFSLYF 75
DB 1 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKGHGLFSLYF 60

QY 76 GSMTPVAVASTPELFLKFLQTHETSFNTRFQTSAIRRLTYDSSVAMVDFGYPWKFVRKL 135
DB 61 GSMTPVAVASTPELFLKFLQTHETSFNTRFQTSAIRRLTYDSSVAMVDFGYPWKFVRKL 120

QY 136 MNDLPNATTVNKLRLPTQOTRKFLRVMAQGAQKPLDTEELLKWTNSTISMMMLGEA 195
DB 121 MNDLPNATTVNKLRLPTQOTRKFLRVMAQGAQKPLDTEELLKWTNSTISMMMLGEA 180

QY 196 EBIROIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREIV 255
DB 181 EBIROIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREIV 240

QY 256 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSAVATEW 315
DB 241 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSAVATEW 300

QY 316 ALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKRK 375
DB 301 ALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKRK 360

QY 376 CTEECINGVYIPEGALIFNNVQVGRDPKVDRESEPRPERFLETGAEGAGPLDLRGQ 435
DB 361 CTEECINGVYIPEGALIFNNVQVGRDPKVDRESEPRPERFLETGAEGAGPLDLRGQ 420

QY 436 HFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEERA 495
DB 421 HFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEERA 480

QY 496 GLTVPRASHSLVCVPLARI 513
DB 481 GLTVPRASHSLVCVPLARI 498

RESULT 17
US-09-857-581-20
; SEQUENCE 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
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; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-20

Query Match      93.3%; Score 2503; DB 1; Length 499;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 483; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 15 FHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKGHGLFSLY 74
DB 1 FHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKGHGLFSLY 60

QY 75 FGSMTPVAVASTPELFLKFLQTHETSFNTRFQTSAIRRLTYDSSVAMVDFGYPWKFVRKL 134
DB 61 FGSMTPVAVASTPELFLKFLQTHETSFNTRFQTSAIRRLTYDSSVAMVDFGYPWKFVRKL 120

QY 135 MNDLPNATTVNKLRLPTQOTRKFLRVMAQGAQKPLDTEELLKWTNSTISMMMLGE 194
DB 121 MNDLPNATTVNKLRLPTQOTRKFLRVMAQGAQKPLDTEELLKWTNSTISMMMLGE 180

QY 195 ABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREI 240

QY 255 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSAVATE 314
DB 241 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSAVATE 300

QY 315 WALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKR 374
DB 301 WALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKR 360

QY 375 KCTEECEINGVYIPEGALIFNNVQVGRDPKVDRESEPRPERFLETGAEGAGPLDLRG 434
DB 361 KCTEECEINGVYIPEGALIFNNVQVGRDPKVDRESEPRPERFLETGAEGAGPLDLRG 420

QY 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 18
US-09-857-581-16
; SEQUENCE 16, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
; US-09-857-581-16

Query Match      92.5%; Score 2482; DB 1; Length 499;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 478; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 15 FLHLRPTAKSALRHLNPPSPKRLPFIHLLHLLKDLHYALIDLSKKGPLFSLY 74
DB 1 FLHLRPTAKSALRHLNPPSPKRLPFIHLLHLLKDLHYALIDLSKKGPLFSLS 60
QY 75 FGSNPTVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVVRKL 134
DB 61 FGSNPTVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVVRKL 120
QY 135 IMNDLPNATTNKLRLPRTQOTRKFLRVMAQAGAAQKPLDLTEELLKWTNSTISMMLGE 194
DB 121 IMNDLPNATTNKLRLPRTQOTRKFLRVMAQAGAAQKPLDLTEELLKWTNSTISMMLGE 180
QY 195 AEIRDIAREVLTIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKDPPVVERVVKRRREI 254
DB 181 AEIRDIAREVLTIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKDPPVVERVVKRRREI 240
QY 255 VRRKNGEVVEGEVSGVFLDTLLEFAEDTMEIKITKDHIIEGLVVDFFSAGTSDTAVATE 314
DB 241 VRRKNGEVVEGEVSGVFLDTLLEFAEDTMEIKITKEQIKGLVVDLFSAGTSDTAVATE 300
QY 315 WALAELINNPKVLEKAREEYVSVGKDRLVDEVDTONLPYIRAIKVTETFRMHPPPLPVVKR 374
DB 301 WALAELINNPKVLEKAREEYVSVGKDRLVDEVDTONLPYIRAIKVTETFRMHPPPLPVVKR 360
QY 375 KCTEECEINGYVPEGALILFNWQGRDPKYWDPSSEPRPERFLETGAEGAGPLDLRG 434
DB 361 KCTEECEINGYVPEGALILFNWQGRDPKYWDPSSEPRPERFLETGAEGAGPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCDFDLQVLGPGQQLKGGDAKVSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCDFDLQVLGPGQQLKGGDAKVSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 19
US-09-857-581-38
; Sequence 38, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: B1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 38
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Trifolium repens
; US-09-857-581-38

Query Match      91.6%; Score 2457; DB 1; Length 498;
Best Local Similarity 95.4%; Pred. No. 0;
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Matches 474; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 17 HLRPTPTAKSALRHLNPPSPKRLPFIHLLHLLKDLHYALIDLSKKGPLFSLYFG 76
DB 2 HLRPTPTAKSALRHLNPPSPKRLPFIHLLHLLKDLHYALIDLSKKGPLFSLSFG 61
QY 77 SMPTVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVVRKLIM 136
DB 62 SMPTVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVVRKLIM 121
QY 137 NDLPNATTNKLRLPRTQOTRKFLRVMAQAGAAQKPLDLTEELLKWTNSTISMMLGEAE 196
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QY 497 LTVPRAHSLVCVPLARI 513
DB 482 LTVPRAHSLVCVPLARI 498

Search completed: March 1, 2004, 07:04:40
Job time : 3 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2004, 16:55:28 ; Search time 1 Seconds

(without alignments)

6.282 Million cell updates/sec

Title: AF022462

Perfect score: 1824

Sequence: 1 GGAAATAGCTCACAAA.....TAAACTATCAATCCTTATAT 1824

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1722 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : af135484.gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1685.9	92.4	1722	1	AF135484 ACCESSION:AF135484

ALIGNMENTS

RESULT 1
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DEFINITION Glycine max cytochrome P450 monooxygenase CYP93C1v2p (CYP93C1v2)
mRNA, complete cds.
ACCESSION AF135484
VERSION AF135484.1 GI:5059123
KEYWORDS
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 1722)
Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
Molecular characterization of the enzyme catalyzing the aryl migration reaction of isoflavonoid biosynthesis in soybean Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
99306846
10375412
2 (bases 1 to 1722)
Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
Direct Submission
Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam Noble Pkwy, Ardmore, OK 73402, USA
LOCATION/Qualifiers
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